

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:22 ; Search time 31 Seconds
(without alignments)
1008.110 Million cell updates/sec

Title: US-10-743-697-1
Perfect score: 2046
Sequence: 1 ELVMTQSPSSLTVTAGEKVT.....LDVWGQGTTLTVSSHHHHH 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCRTUS-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1484.5	72.6	495	US-09-948-004-18	Sequence 18, Appl
2	1287.5	62.9	553	US-08-263-911-9	Sequence 9, Appl
3	1283	62.7	483	US-08-392-338A-19	Sequence 19, Appl
4	1283	62.7	483	US-09-166-750-19	Sequence 19, Appl
5	1283	62.7	483	US-09-166-093-19	Sequence 19, Appl
6	1283	62.7	483	US-09-172-019-19	Sequence 19, Appl
7	1283	62.7	483	US-09-166-094-19	Sequence 19, Appl
8	1283	62.7	483	US-09-443-213-19	Sequence 19, Appl
9	1230.5	60.1	553	US-08-263-911-7	Sequence 7, Appl
10	955	45.7	456	US-09-495-880A-11	Sequence 11, Appl
11	938	45.8	249	US-09-069-821-2	Sequence 2, Appl
12	938	45.8	249	US-09-956-086-2	Sequence 2, Appl
13	938	45.8	249	US-09-393-627B-28	Sequence 28, Appl
14	937	45.8	354	US-09-420-592A-2	Sequence 2, Appl
15	937	45.8	257	US-09-985-442-2	Sequence 2, Appl
16	937	45.8	257	US-09-983-580-4	Sequence 4, Appl
17	937	45.8	257	US-09-791-540-4	Sequence 4, Appl
18	937	45.8	257	US-09-791-540-6	Sequence 4, Appl
19	937	45.8	257	US-09-791-540-4	Sequence 4, Appl
20	937	45.8	269	US-09-420-592A-4	Sequence 4, Appl
21	937	45.8	269	US-09-985-442-4	Sequence 4, Appl
22	937	45.8	269	US-09-983-580-4	Sequence 4, Appl
23	937	45.8	269	US-09-791-540-6	Sequence 4, Appl
24	937	45.8	269	US-09-791-540-4	Sequence 4, Appl
25	937	45.8	269	US-09-791-540-4	Sequence 4, Appl
26	937	45.8	269	US-08-323-445A-4	Sequence 4, Appl
27	937	45.8	269	US-08-315-903A-4	Sequence 4, Appl

28	928.5	45.4	553	US-08-661-052-16	Sequence 16, Appl
29	928.5	45.4	553	US-09-188-082-16	Sequence 16, Appl
30	928.5	45.4	553	US-09-364-088-16	Sequence 16, Appl
31	928.5	45.4	553	US-09-102-716-16	Sequence 16, Appl
32	927	45.3	246	US-09-791-540-2	Sequence 2, Appl
33	927	45.3	246	US-09-791-540-2	Sequence 2, Appl
34	925	45.2	264	US-08-323-445A-8	Sequence 8, Appl
35	925	45.2	264	US-08-515-903A-8	Sequence 8, Appl
36	925	45.2	264	PCT-US95-12840-8	Sequence 8, Appl
37	894.5	43.7	275	US-08-463-903-8	Sequence 8, Appl
38	894.5	43.7	275	US-07-935-695-8	Sequence 8, Appl
39	890.5	43.5	275	US-08-463-903-17	Sequence 17, Appl
40	890.5	43.5	275	US-07-935-695-17	Sequence 17, Appl
41	890.5	43.5	280	US-08-463-903-10	Sequence 10, Appl
42	890.5	43.5	280	US-07-935-695-10	Sequence 10, Appl
43	890.5	43.5	282	US-08-463-903-12	Sequence 12, Appl
44	890.5	43.5	282	US-08-463-903-15	Sequence 15, Appl
45	890.5	43.5	282	US-07-935-695-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1					
US-09-948-004-18					
Sequence 18, Application US/09948004					
Patent No. 6723538					
GENERAL INFORMATION:					
APPLICANT: MACK, Mathias					
TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in					
TITLE OF INVENTION: Immunological disorders					
FILE REFERENCE: E 2411 EP					
CURRENT APPLICATION NUMBER: US/09/948,004					
CURRENT FILING DATE: 2001-09-05					
NUMBER OF SEQ ID NOS: 34					
SOFTWARE: PatentIn Ver. 2.1					
SEQ ID NO 18					
LENGTH: 495					
TYPE: PRT					
ORGANISM: Mus sp.					
US-09-948-004-18					
Query Match					
Best Local Similarity 74.7% Pred. No. 2.4e-102; Length 495;					
Matches 278; Conservative 34; Mismatches 53; Indels 7; Gaps 2;					
QY	1	ELVMTQSPSSLTVTAGEKVTMSCKSSQSLNSGNOKYLTWYQKPGQPKLLIYASTR	60		
DB	1	DIVLTQSPASLSASVGEIVTITCRASENII-----SYLAWYQKQKSPOLLVYNAKTL	54		
QY	61	ESGVDPRTFGSGGTFDTLTSSVOAEDLAVYYCONDYSPITFGAGTLEIKGGGSGG	120		
DB	55	TGVFSRFGSGSGGTQFSLKINSIQPEDFGNFCOHYDTPPTFGGTLEIKGGGSGG	114		
QY	121	GGSGGGSGSVOLLESGAEIYRPGTSVYKISCKASGAFTNYLGMWKORPGHLEWIGDI	180		
DB	115	GGSGGGSGSVQV-LQDPGAGRVRPGASVSKLSCASGYSFISMMNWKORPGGLEWIGDI	173		
QY	181	PGSGNIHNEKFKKATLTADKSSSTAYMQLSLTFEDSAVYFCARLNMDEPDYWGQ	240		
DB	174	HSDSETRNQNKFNRATITVDKYSTAVIQQLSPFSEDSAVYFCARGEYIGIFDYWGQ	233		
QY	241	GTTVTYSSGGGSDIKLQSGAEIARPGASVYKISCKTSYTRTYMHVWKORPGGLEW	300		
DB	234	GTTVTYSSGGGSDIKLQSGAEIARPGASVYKISCKTSYTRTYMHVWKORPGGLEW	293		
QY	301	IGYINPREGTYNNOKFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYYDDHYCD	360		
DB	294	IGYINPREGTYNNOKFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYYDDHYCD	353		
QY	361	YWGQGTTLTVSS 372			
DB	354	YWGQGTTLTVSS 365			

```

RESULT 2
US-08-263-911-9
Sequence 9, Application US/08263911
Patent No. 5877291
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S
APPLICANT: Gouille, Brian B
TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/263,911
FILING DATE: 21-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,263
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ulmer, Duane C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-41,014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Protein
LOCATION: 23
US-08-263-911-9

Query Match      62.9%; Score 1287.5; DB 1; Length 553;
Best Local Similarity    64.2%; Pred. No. 1.1e-87;
Matches 258; Conservative   37; Mismatches 68; Indels 39; Gaps 5;

QY      1 ELWMTQSSSLTVTAGEKYTMSCKSSGSLNSGNKNLTLYQQKPGQPPLTIITMASTR 60
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      23 DIVMSQSSSLSPVSGEKVTLSCKSSQSLVSGNKNLTAMVQQKPGSPKLTIYMASAR 82
QY      61 ESGVPDRFTGSAGSGDFTLTTISVVAEDLAAYVCNDYSYPFLTFAGTKLEIKGGGSGG 120
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      83 ESGVPDRFTGSAGSGDFTLTTISSVATEDLAYVYCQYYSYPLTFAGTKLVAKLSADAK 142
QY      121 GSGGGGGG-----EVQLLEDSGAELVRPGETSVKISCKASGYAFTNWLGAVKORP 170
       :|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      143 KDAKKDDAKDKADKADKELEVQ-LQSDDELVPGLASVIKCAASYPTLDHAIHWKONP 201
QY      171 GHGLEWIDIPFGSGSNHYHNKEFKGKATLLTDKSSTVMQLSSTFFDSAAVFCARLRN 230
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      202 EGGLEWMIGYGFBNDFPKNERFKKATLTADKSSIAIVQLNSLTSESAAYVFTRLRN 261
QY      231 WDEPDMDYGQGTTTVVSSGGGGS-----DIKLQSGAEIARPGAS 270
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      262 ----MAYVGQGRSVTVSSLSADAKKADKADKADKADKADKDLENVQLQSDDELVKPGAS 317
QY      271 VMGSKTSIGYFTTRVTMMVYKORPPQGLEWIGYINPSRGYNTRYNOKFQDKATLTITDKSS 330
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Db      318 VKISCKASGTTFTFDHAIHWKQNPBGQLEWIGFSPENDPFCKNERKKGATLTLDKSSS 372
Qy      331 TAYWQSLTSEDSAVYTCARYDDHCLDYGQGTTLTVSS 372
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      378 TAYVQLNLSLTSEDSAVYFCTTRSIN---MAYWQGTISVTSS 415

RESULT 3
US-08-392-338A-19
/ Sequence 19, Application US/08392338A
/ Patent No. 5869620
/ GENERAL INFORMATION:
/ APPLICANT: Whitlow, Marc
/ APPLICANT: Wood, James F.
/ APPLICANT: Hardman, Karl
/ APPLICANT: Bird, Robert
/ APPLICANT: Filpula, David
/ TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
/ STREET: 1100 New York Avenue, NW
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/392,338A
/ FILING DATE: 22-FEB-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/989,846
/ FILING DATE: 20-NOV-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/796,936
/ FILING DATE: 25-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Goldstein, Jorge A.
/ REGISTRATION NUMBER: 29,021
/ REFERENCE/DOCKET NUMBER: 0977.0030007
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 483 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-392-338A-19

Query Match      62.7%; Score 1283; DB 1; Length 483;
Best Local Similarity 53.8%; Pred. No. 2,1e-87;
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

Qy      1 ELVWTGSSSLFTVWAGERVTVMSCKSSQSLNSGNQKRYLTVYQKRPQGPPLTLTYMASTR 60
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 DVNWSQSPSSLPVSVGKERVTLSCKSQSSQLLYSGNQKNYLMWYQKPPQSPPLTLTYMASAR 60
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      61 ESGVPDSEFTFGSGSTDTFTLTSSVQABDLAVYVQNDYSYPLTFGAGTKLEIKGGGSGG 120
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 ESGVPDRFTFGSGSTDTFTLTSSVKTEDLAVYTCQYYSPLTFGAGTKLVK-GSTRGS 119
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      121 GSGSGGGSSEVQLLEQSGAEIVRPETSVKISCKASGVAFTYVWLMGVORPGHGLEWIGDI 180
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      120 GKSEBGKGVQV-LOQSDAEIVKPGASVKISCKASGFTFDHAIHWKQNPBGQLEWIGYF 178
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      181 PFGSGNHVNEKEFKGKATLTLDKSSSTRAVWQLSLTDEDSAVYFCARLRWDEMDYTWQ 240
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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Db 179 SPGNDDEKYNRFRKATLTADKSSSTAYVOLNSLTSBDSAVYFCTRLSLN----MAYWGQ 234
QY 241 GTTATVSS----- 248
Db 235 GTSTVSSDVMMSQSPSSLPVSGEKYTLSCKSSQSLVSGNQKYLAWYQKPGQSPKL 294
QY 249 -----GGGGSQD----- 254
Db 295 LIYMASARESGVPDRFTSGSGGTDTFTLSSVKTEDLAVYYCOQYYSYPLTFGAGTKLVL 354
QY 255 -----ITLQSGAEIAPPGASVKNKSCSTSGYTFRTYTMHWKORPGQGL 298
Db 355 KGSTSGSKSGSEKGQVQLQSDAEIVKPGASVKISCKASGTYFTDHAHWKONPEQGL 414
QY 299 EMIGYINPSRGYTNYNQKFKKATLTITDKSSSTAYMQLSLTSBDSAVYYCARYYDDHYC 358
Db 415 EMIGYFSPGNDDEKYNRFRKATLTADKSSSTAYVOLNSLTSBDSAVYFCTRLSLN---- 470
QY 359 LDYWGQGTTLTVS 371
Db 471 MAYWGQGTSTVVS 483

RESULT 4
US-09-166-750-19
Sequence 19, Application US/09166750
Patent No. 6025165

GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rolence, Michelle
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,750
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-166-750-19

Query Match 62.7%; Score 1283; DB 2; Length 483;
Best Local Similarity 53.8%; Pred. No. 2,18-87;
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVMTQSPSSSLITVAGEKVTMSCKSSQSLNSGNQKYLTYOQKPGQPRFLITLTMATR 60
Db 1 DVNMSQSPSSLPVSGEKYTLSCKSSQSLVSGNQKYLAWYQKPGQSPKLITLTMASAR 60
QY 61 ESSGVPDRFTSGSGGTDTFTLTSVQAEIAPPGASVKNKSCSTSGYTFRTYTMHWKORPGHLEWIDT 180
Db 61 ESSGVPDRFTSGSGGTDTFTLTSVQAEIAPPGASVKNKSCSTSGYTFRTYTMHWKORPGHLEWIDT 180
QY 121 GSGSGSGSEVQLLQSGAEIVRPGTSVKISCKASGYAFTHYMLGWKORPGHLEWIDT 180
Db 120 GKSSEKQGVQ-LQSDAEIVKPGASVKISCKASGYFTDHAHWKONPEGLEWIGYF 178
QY 181 FPGSGNIHNEKFKKATLTADKSSSTAYMQLSLTFEDSAVYPCARLRNDEPYDHYCQ 240
Db 179 SPGNDDEKYNRFRKATLTADKSSSTAYVOLNSLTSBDSAVYFCTRLSLN----MAYWGQ 234
QY 241 GTTATVSS----- 248
Db 235 GTSTVSSDVMMSQSPSSLPVSGEKYTLSCKSSQSLVSGNQKYLAWYQKPGQSPKL 294
QY 249 -----GGGGSQD----- 254
Db 295 LIYMASARESGVPDRFTSGSGGTDTFTLSSVKTEDLAVYYCOQYYSYPLTFGAGTKLVL 354
QY 255 -----ITLQSGAEIAPPGASVKNKSCSTSGYTFRTYTMHWKORPGQGL 298
Db 355 KGSTSGSKSGSEKGQVQLQSDAEIVKPGASVKISCKASGTYFTDHAHWKONPEQGL 414
QY 299 EMIGYINPSRGYTNYNQKFKKATLTITDKSSSTAYMQLSLTSBDSAVYYCARYYDDHYC 358
Db 415 EMIGYFSPGNDDEKYNRFRKATLTADKSSSTAYVOLNSLTSBDSAVYFCTRLSLN---- 470
QY 359 LDYWGQGTTLTVS 371
Db 471 MAYWGQGTSTVVS 483

RESULT 5
US-09-166-093-19
Sequence 19, Application US/09166093
Patent No. 6027725

GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rolence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,093

FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977,003000B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-166-093-19

Query Match 62.7%; Score 1283; DB 2; Length 483;
Best Local Similarity 53.8%; Pred. No. 2,1e-87;
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVNTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
DB 1 DVVMSGSPSSLPVSVGEKVTLSCKSSQSLNSGNQKNYLTWYQKPGQSPKLLIYMASAR 60
QY 61 ESVGPRDFTGSGGSDTFTLTSSVQAEADLAIVYCONDYSYPLTFGAGTKLEIKGGGSGG 120
DB 61 ESVGPRDFTGSGGSDTFTLTSSVQAEADLAIVYCONDYSYPLTFGAGTKLVK-GSTSGS 119
QY 121 GSGSGGSEVQLLEFGSAELVPRGTSYKISCKASGYFTNWLGWVKORPGHLEWIGDI 180
DB 120 GKSSEGGKQVO-LQOSDAELVPRGASVYKISCKASGYFTDHAIHVWKNPEQGLEWIGYF 178
QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRWDEPDYWGQ 240
DB 179 SPGNDPFKNRFRKATLTADKSSSTAYWQLSLTFEDSAVYFCRSLN---MAYWQ 234
QY 241 GTTYVSS----- 248
DB 235 GTSVTSSDVVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKNYLTWYQKPGQSPKL 294
QY 249 -----GGGSD----- 254
DB 295 LIYMASARESGVPRDFTGSGGSDTFTLTSSVQAEADLAIVYCONDYSYPLTFGAGTKLV 354
QY 255 -----IKLQOSGAELVPRGASVYKISCKASGYFTTRYTMWVKORPGQL 298
DB 355 KGTSGSGKSEGGKQVO-LQOSDAELVPRGASVYKISCKASGYFTDHAIHVWKNPEQGL 414
QY 299 EMIGVINPSRGTYNQKFKATLTADKSSSTAYWQLSLTFEDSAVYFCARLYDDHYC 358
DB 415 EMWYFSPGNDPFKNRFRKATLTADKSSSTAYWQLSLTFEDSAVYFCRSLN--- 470
QY 359 LDYWGQGTTLTVS 371
DB 471 MAYWQGTSTVTS 483

RESULT 6
US-09-172-019-19
Sequence 19, Application US/09172019
Patent No. 6103889
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc

APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,019
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977,003000D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-172-019-19

Query Match 62.7%; Score 1283; DB 2; Length 483;
Best Local Similarity 53.8%; Pred. No. 2,1e-87;
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVNTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
DB 1 DVVMSGSPSSLPVSVGEKVTLSCKSSQSLNSGNQKNYLTWYQKPGQSPKLLIYMASAR 60
QY 61 ESVGPRDFTGSGGSDTFTLTSSVQAEADLAIVYCONDYSYPLTFGAGTKLEIKGGGSGG 120
DB 61 ESVGPRDFTGSGGSDTFTLTSSVQAEADLAIVYCONDYSYPLTFGAGTKLVK-GSTSGS 119
QY 121 GSGSGGSEVQLLEFGSAELVPRGTSYKISCKASGYFTNWLGWVKORPGHLEWIGDI 180
DB 120 GKSSEGGKQVO-LQOSDAELVPRGASVYKISCKASGYFTDHAIHVWKNPEQGLEWIGYF 178
QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRWDEPDYWGQ 240
DB 179 SPGNDPFKNRFRKATLTADKSSSTAYWQLSLTFEDSAVYFCRSLN---MAYWQ 234
QY 241 GTTYVSS----- 248
DB 235 GTSVTSSDVVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKNYLTWYQKPGQSPKL 294
QY 249 -----GGGSD----- 254
DB 295 LIYMASARESGVPRDFTGSGGSDTFTLTSSVQAEADLAIVYCONDYSYPLTFGAGTKLV 354

[illegible]

```

RESULT 7
US-09-166-094-19
; Sequence 19, Application US/09166094
; Patent No. 6121424
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,094
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-166-094-19

Query Match 62.7%; Score 1283; DB 2; Length 483;
Best Local Similarity 53.8%; Pred. No. 2,1e-87;
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6

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Db      1  DVWMSQSPSSLPVSGEKVTLTSCKSQGLTSLXGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Qy      61  ESGVPRPTGSGSGTDFLTLTSSVOAEDLAVYYCONDYSPLTFGAGTLEIKGGGSGSG 120
Db      61  ESGVPRPTGSGSGTDFLTLTSSVKTEDLAVYYCOQYISPLTFGAGTKVLK-GTSGS 119
Qy      121  GSGSGGSGSEVOLLTSGSGAELVPRGTSVKISCKASGYAEFTNWLGMVKRPGHGLEWIGDI 180
Db      120  GKSSEGNQYQV-LQSDAELVKPGASVKISCKASGYTFTHDAIHWKQNPQEGLEWIGYF 178
Qy      181  PPSGNIHYNKEFKGKATLTADKSSSTAYMQLSSTLPFSDSAVYFCARLKNMBEPMQWMO 240
Db      179  SPGNDDPFKYNRPFKQKATLTADKSSSTAYVQLNLSLTSBDSAVYFCTRSLN---MAYWG 234
Qy      241  GTVTYVSS----- 248
Db      235  GTSVTVSSDVWMSQSPSSLPVSGEKVTLTSCKSQGLTSLXGNQKNYLAWYQKPGQSPKL 294
Qy      249  -----GGGGSDF----- 254
Db      295  LIYWASARESGVPRFTGSGSGTDFLTLTSSVKTEDLAVYYCOQYISPLTFGAGTKVL 354
Qy      255  -----IKLQSGAELARPASGVKMSCKTSGYTFRTYRTHMHWKQRPQGL 298
Db      355  KGSTSGSGKSGSEGNQYQLQSDALVLRPGASVKISCKASGYTFTHDAIHWKQNPQEGGL 414
Qy      299  EMIGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSSTLPSEDSAVYICARYDDHYC 358
Db      415  EMIGYFSPGNDDPFKYNRPFKQKATLTADKSSSTAYVQLNLSLTSBDSAVYFCTRSLN--- 470
Qy      359  LDYWGQGTITLV 371
Db      471  MAYWGQGTITLV 483

```

RESULT 8
 US-09-443-213-19
 / Sequence 19, Application US/09443213
 / Patent No. 6515110
 / GENERAL INFORMATION:
 / APPLICANT: Whitlow, Marc
 / APPLICANT: Wood, James F.
 / APPLICANT: Hardman, Karl
 / APPLICANT: Bird, Robert
 / APPLICANT: Filpula, David
 / APPLICANT: Rollence, Michelle
 / TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
 / NUMBER OF SEQUENCES: 23
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Sterne, Kessier, Goldstein & Fox P.L.L.C.
 / STREET: 1100 New York Avenue, NW
 / CITY: Washington
 / STATE: D.C.
 / COUNTRY: U.S.A.
 / ZIP: 20005
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/443,213
 / FILING DATE: Herewith
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 09/166,094
 / FILING DATE: 05-OCT-1998
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/392,338
 / FILING DATE: 22-FEB-1995
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/989,846
 / FILING DATE: 20-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977, 003000E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-443-213-19

Query Match 62.7%; Score 1283; DB 2; Length 483;
Best Local Similarity 53.8%; Pred. No. 2.1e-87;
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVNTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKXLTWYQKPGQPKLLIYMASTR 60
DB 1 DVVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKXLTWYQKPGQPKLLIYMASAR 60
QY 61 ESVGPRFTSGSGTDTLTLSISVQAEFLAVYCONDYSPYLPFGAGTKLEIKGGGSGG 120
DB 61 ESVGPRFTSGSGTDTLTLSISVQAEFLAVYCONDYSPYLPFGAGTKLVK-GSTSGS 119
QY 121 GSGGSGGSEVOLLEQSGAEIVRPQTSVKISCKASGYAFTNYMLGMVQKPGHLEWIGDI 180
DB 120 GKSSBKGGQVQ-LQOSDAELVKPGASVKISCKASGYFTDHAIHVWQNPFGLEWIGYF 178
QY 181 FPGSGNIHNEKEFGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLNDPEMDYMCQ 240
DB 179 SPGNDPFRYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRLN----MAYWQ 234
QY 241 GTVTYVSS----- 248
DB 235 GTSVTVSSDVVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKXLTWYQKPGQSPKL 294
QY 249 -----GGGGS- 254
DB 295 LIYMASRESGVPDRFTSGSGTDTLTLSISVQTEDLAVYCCQYYSYLPFGAGTKLV 354
QY 255 -----IKLQOSGAELARPASVMSCTSGYTRTYMHWKQRPQGL 298
DB 355 KGSTSGSKSEGGQVQLQOSDAELVKPGASVKISCKASGYFTDHAIHVWQNPFGGL 414
QY 299 EMIGYINPSRGYTNVNOFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYC 358
DB 415 EMIGYINPSRGYTNVNOFKDKATLTDDKSSSTAYVQLNSLTSEDSAVYFCTRLN---- 470
QY 359 LDYMGQGTTLTVS 371
DB 471 MAYWGGGTSTVVS 483

RESULT 9
US-08-263-911-7
Sequence 7, Application US/08263911
Patent No. 5877291
GENERAL INFORMATION:
APPLICANT: Mezei, Peter S
APPLICANT: Goutille, Brian B
TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI

COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/263,911
FILING DATE: 21-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,263
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ulmer, Duane C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-41,014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Protein
LOCATION: 23
US-08-263-911-7

Query Match 60.1%; Score 1230.5; DB 1; Length 553;
Best Local Similarity 48.3%; Pred. No. 1.9e-83;
Matches 261; Conservative 37; Mismatches 65; Indels 177; Gaps 6;

QY 1 ELVNTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKXLTWYQKPGQPKLLIYMASTR 60
DB 23 DVVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKXLTWYQKPGQSPKLIIYMASAR 82
QY 61 ESVGPRFTSGSGTDTLTLSISVQAEFLAVYCONDYSPYLPFGAGTKLEIKGGGSGG 120
DB 83 ESVGPRFTSGSGTDTLTLSISVQAEFLAVYCONDYSPYLPFGAGTKLVKLSADDAK 142
QY 121 GSGGSGGSEVOLLEQSGAEIVRPQTSVKISCKASGYAFTNYMLGMVQK 170
DB 143 KDAKDKDAKDKDAKDKDLVQ-LQOSDAELVKPGASVKISCKASGYFTDHAIHVWQNP 201
QY 171 GHGLEWIGDIFPQSGNIHNEKEFGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLN 230
DB 202 EQGLEWIGYFSPGNDPFRYNERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRLN 261
QY 231 WDFEMDYMGQGTTLTVS----- 248
DB 262 ----MAYWGGGTSTVVSLSADDAKDAKDAKDKDAKDKDLIVMSQSPSSLPVSVGB 317
QY 249 -----GGGGS- 254
DB 318 KVTLSCKSSQSLNSGNQKXLTWYQKPGQSPKLIIYMASARESVPDRFTSGSGTDF 377
QY 255 ----- 254
DB 378 TLISVQTEDLAVYCCQYYSYLPFGAGTKLVKLSADDAKDAKDAKDKDAKDKD 437
QY 255 --IKLQOSGAELARPASVMSCTSGYTRTYMHWKQRPQGLEWIGYINPSRGYTN 312
DB 438 LEVQLQOSDAELVKPGASVKISCKASGYFTDHAIHVWQNPFGLEWIGYFSGNDPDK 497
QY 313 YNOFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCUDYMGQGTTLTVS 372
DB 498 YNERFKKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRLN----MAYWGGGTSTVVS 553

RESULT 10

RESULT 14
US-09-393-627B-28
Sequence 28, Application US/09393627B
Patent No. 6455314
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Kovacs, Imre
APPLICANT: Roelivink, Petrus W.
APPLICANT: Bruder, Joseph T.
TITLE OF INVENTION: Alternatively Targeted Adenovirus
FILE REFERENCE: 202345
CURRENT APPLICATION NUMBER: US/09/393,627B
CURRENT FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/099,851
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: US 60/136,529
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent In Ver. 2.2
SEQ ID NO 28
LENGTH: 354
TYPE: PRT
ORGANISM: Anti-HA ScFv fused in frame with 2 C-terminal myc epitopes and
PDGF receptor transmembrane anchor (Anti-HA pseudo-receptor)
US-09-393-627B-28

Query Match 45.8%; Score 938; DB 2; Length 354;
Best Local Similarity 71.3%; Pred. No. 5.8e-62;
Matches 179; Conservative 28; Mismatches 40; Indels 4; Gaps 3;

QY 1 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLINSGNQKNTLTWYQKPGQPPKLLIYMASTR 60
DB 27 DIVMTQSPSSSLTVTAGEKVTMSCKSSQSLINSGNQKNTLTWYQKPGQPPKLLIYMASTR 86
QY 61 ESGVDRFTGSGSGDTFTLTSSVQAEADLAVYYCQNDYSYPLTFGAGTKLEIK--GGGGS 118
DB 87 ESGVDRFTGSGSGDTFTLTSSVQAEADLAVYYCQNDYSYPLTFGAGTKLEIKRAAGGGS 146
QY 119 GGGSGGGGSEVQLLEQSGAEIVRPQTSYKISCKASGYAFITNYMLGWYKORPGHLEWIG 178
DB 147 GGGSGGGGSEVQLLEQSGAEIVRPQTSYKISCKASGYAFITNYMLGWYKORPGHLEWVP 205
QY 179 DIPGSGNIHNEKFKGKATLTADKSSSTAYVQSLTFEDSAVYFCARLRNWDPE-MDY 237
DB 206 TIIRGSGYTYYPDSYKREFTISKNNAKNTLYLQMSLSKEDTAYMYCARETFDEKGFAY 265
QY 238 WGQGTIVTVSS 248
DB 266 WGQGTIVTVSA 276

RESULT 15
US-09-420-592A-2
Sequence 2, Application US/09420592A
Patent No. 6333396
GENERAL INFORMATION:
APPLICANT: Filpula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300001
CURRENT APPLICATION NUMBER: US/09/420,592A
CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 257
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 scFv

US-09-420-592A-2

Query Match 45.8%; Score 937; DB 2; Length 257;
Best Local Similarity 74.3%; Pred. No. 4.7e-62;
Matches 185; Conservative 22; Mismatches 36; Indels 6; Gaps 3;

QY 1 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLINSGNQKNTLTWYQKPGQPPKLLIYMASTR 60
DB 1 DIVMTQSPSSSLTVTAGEKVTMSCKSSQSLINSGNQKNTLTWYQKPGQPPKLLIYMASTR 60
QY 61 ESGVDRFTGSGSGDTFTLTSSVQAEADLAVYYCQNDYSYPLTFGAGTKLEIKG--GGG 119
DB 61 ESGVDRFTGSGSGDTFTLTSSVQAEADLAVYYCQNDYSYPLTFGAGTKLEIKGSGSG 120
QY 120 GGGSGGGGSEVQLLEQSGAEIVRPQTSYKISCKASGYAFITNYMLGWYKORPGHLEWIG 178
DB 121 KPGSGEGSTKQVQLQDSGAEIVRPQTSYKISCKASGYAFITDHAHWKQNPQGLEWIG 180
QY 179 DIPGSGNIHNEKFKGKATLTADKSSSTAYVQSLTFEDSAVYFCARLRNWDPEMDY 238
DB 181 YFSPENDDFKTYNEKFKGKATLTADKSSSTAYVQSLTSEDSAVYFCTRSIN---MAYW 236
QY 239 GQGTIVTVS 247
DB 237 GQGTIVTVS 245

Search completed: March 6, 2006, 13:14:16
Job time : 32 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:22 ; Search time 25 Seconds
(without alignments)
1454.797 Million cell updates/sec

Title: US-10-743-697-1

Perfect score: 2046
Sequence: 1 ELVMTGSPSSLTVTAGEKVT.....LDYWGQGTTLTVSSHHHHH 378

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	30.8	287	4 PC4402	pe1b leader/Ig hea
2	576	28.2	113	2 PLO263	Ig kappa chain V r
3	563.5	27.5	220	2 A31790	Ig kappa chain V r
4	548	26.8	112	2 F30538	Ig kappa chain V r
5	545	26.6	112	2 E30538	Ig kappa chain V r
6	539	26.3	113	2 PLO264	Ig kappa chain V r
7	532	26.0	108	2 E30535	Ig kappa chain V r
8	532	26.0	135	2 S38807	Ig light chain V-J
9	530.5	25.9	139	2 P80024	Ig heavy chain pre
10	527	25.8	107	2 G30535	Ig kappa chain V r
11	524	25.6	107	2 F30535	Ig kappa chain V r
12	520	25.4	107	2 D30535	Ig kappa chain V r
13	520	25.4	107	2 B30535	Ig kappa chain V r
14	512	25.0	268	2 A56446	Ig heavy chain V r
15	507	24.8	105	2 C30535	Ig kappa chain V r
16	507	24.8	140	2 PH1482	Ig heavy chain V r
17	503	24.6	113	2 A49260	antitumor monoclon
18	502.5	24.6	118	2 PT0356	Ig kappa chain V r
19	502.5	24.6	139	2 A27609	Ig heavy chain pre
20	500	24.4	140	1 HNM5G7	Ig heavy chain pre
21	499.5	24.4	120	2 S41394	Ig heavy chain V r
22	499.5	24.4	131	2 S66337	Ig heavy chain V r
23	499.5	24.4	249	2 S41374	single chain Fv an
24	497.5	24.3	138	2 S26040	Ig kappa chain pre
25	496	24.2	145	2 PLO014	Ig kappa chain pre
26	495.5	24.2	112	2 PLO065	Ig kappa chain V r
27	495.5	24.2	214	2 S68212	Ig kappa chain (Ma
28	494.5	24.2	240	2 S06084	Ig kappa chain pre
29	494	24.1	140	2 PH1489	Ig heavy chain V r

30	492	24.0	246	2 S38950	Ig gamma chain - m
31	492	24.0	446	2 S40295	Ig gamma-2a chain
32	490.5	24.0	120	2 B22769	Ig heavy chain V r
33	490	23.9	140	2 PH1484	Ig heavy chain V r
34	489.5	23.9	139	1 MHMS18	Ig heavy chain pre
35	488.5	23.9	122	2 S24287	Ig heavy chain V r
36	488	23.9	118	2 S38565	Ig heavy chain V r
37	487.5	23.8	112	2 S43103	Ig kappa chain V-J
38	487	23.8	120	2 S25175	Ig heavy chain V r
39	486.5	23.8	112	2 S09970	Ig kappa chain V-J
40	486	23.8	121	2 A26405	Ig heavy chain V r
41	485	23.7	140	2 PH1488	Ig heavy chain V r
42	484.5	23.7	112	2 S41393	Ig kappa chain V r
43	484.5	23.7	115	2 A56700	Ig heavy chain (an
44	484	23.7	140	2 PH1498	Ig heavy chain V r
45	484	23.7	141	2 A39276	Ig heavy chain pre

ALIGNMENTS

RESULT 1
PC4402
pe1b leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
C:Species: synthetic
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C:Accession: PC4402
R:Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997
A:Title: Construction, bacterial expression, and characterization of hapten-specific sin
A:Reference number: PC4402
A:Accession: PC4402
A:Molecule type: DNA
A:Residues: 1-287 <SU2>
A:Cross-references: UNIPARC:UPI000017CF08
C:Keywords: fusion protein

Query Match 30.8%, Score 631, DB 4, Length 287;
Best local similarity 52.5%, Pred. No. 1.6e-33;

Matches 138; Conservative 25; Mismatches 78; Indels 22; Gaps 6;

QY	1	ELVMTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKXLYTVYQKRGQPKLLIYMASTR	60
DB	26	QAVVTQF-SALTTSGEFTVLTCSRSTGAVTT---SNYANVQKRPDLFTGLIGTNNR	81
QY	61	ESGVPRFRTSGSGSGTDFLTITSSVQAEPLAVYYCONDYSYPLTFGATKLEI-----	112
DB	82	APGVPRFRTSGSLIGDKALTTITGAQTEDEALYFCALMYSNMHVFGGRTKLTFLSSADPAK	141
QY	113	-----KGGGGGGGGGGGGSEVQLLEQSGAEIVRPGTSYKISCSASGYAFNNYLGWYK	167
DB	142	KDDAKKDDPAKKDDAKKDG---QVQ-LQPGAEIVRPGASVKLSCASGTFSTYMHVWK	197
QY	168	ORPGHGLEWIGDIPFGSGNIHYNKFKGKATLTADKSSSTAYMQSLTFEDSAVYFCAR	227
DB	198	QPGKGLWIGITIDNSGCTKNEFKSKATITVDKPSSTAYMQSLTSEDSAVYICAR	257
QY	228	LRNMDP-MDYWGQGTTLTVSSG	249
DB	258	VDYGSYFDYWGQGTTLTVSSG	280

RESULT 2
PLO263
Ig kappa chain V region (anti-DNA, S57YK, S41YK, S54YK, S7YK and S204YK) - mouse (Irrgme
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PLO263
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisecky, D.; Marshak-Rothstein, J
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PLO231; MUID:90111618; PMID:2104919
A:Accession: PLO263

A:Molecule type: mRNA
A:Residues: 1-113 <SHL>
A:Cross-references: UNIPARC:UPI0000176AF7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-96/Domain: immunoglobulin homology <IMM>
F:24-40/Region: complementarity-determining 1
F:41-55/Region: complementarity-determining 2
F:56-62/Region: complementarity-determining 2
F:63-94/Region: framework 3
F:95-103/Region: complementarity-determining 3
F:104-113/Region: framework 4

Query Match 28.2%; Score 576; DB 2; Length 113;
Best Local Similarity 96.5%; Pred. No. 1.9e-30;
Matches 109; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60
Db 1 DIVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60

Qy 61 ESGVPRFTGSGSGTDFTLTISVQAEADLAIVYCCNDYSYPLTFGAGTKLEIK 113
Db 61 ESGVPRFTGSGSGTDFTLTISVQAEADLAIVYCCNDYSYPLTFGAGTKLEIK 113

RESULT 3
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C/Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an anti-
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: UNIPARC:UPI0000114E12; GB:M23626; GB:J04061; NID:G533234; PIRN:AAA39
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 27.5%; Score 563.5; DB 2; Length 220;
Best Local Similarity 52.3%; Pred. No. 2.5e-29;
Matches 123; Conservative 19; Mismatches 48; Indels 45; Gaps 5;

Qy 1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60
Db 1 DIVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60

Qy 61 ESGVPRFTGSGSGTDFTLTISVQAEADLAIVYCCNDYSYPLTFGAGTKLEIKGGGSGG 120
Db 61 ESGVPRFTGSGSGTDFTLTISVQAEADLAIVYCCNDYSYPLTFGAGTKLEIK----- 113

Qy 121 GSGSGGSEVQVLLDSGAEIVRPGTSVKISCKAGYAFNTWLGWQKRPBGHEMIGDI 180
Db 114 --RADAPTVSIFPPSSSOLTSGASV-----VCFLNPF 145

Qy 181 PRGSNIHY----NEKFKGKATLTADK--SSSTAVYQQLSLT-----FDSAIVYPC 225
Db 146 YPKDINVMKIDGSEKQGVLSNWTDDSKDYSMSSTLTLTLDYERHNSYTC 200

RESULT 4
F30538
Ig kappa chain V region (253.15D10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C/Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C/Accession: F30538
R:Claflin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A:Reference number: A30534; MUID:89035545; PMID:3141511
A:Accession: F30538
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A:Molecule type: mRNA
A:Residues: 1-112 <CLA>
A:Cross-references: UNIPARC:UPI0000176CD5
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 26.8%; Score 548; DB 2; Length 112;
Best Local Similarity 92.9%; Pred. No. 1.1e-28;
Matches 104; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60
Db 1 DIVWTGSPSSLTVSAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYGASTR 60

Qy 61 ESGVPRFTGSGSGTDFTLTISVQAEADLAIVYCCNDYSYPLTFGAGTKLEI 112
Db 61 ESGVPRFTGSGSGTDFTLTISVQAEADLAIVYCCNDHSYPLTFGAGTKLEI 112

RESULT 5
E30538
Ig kappa chain V region (253.12D3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C/Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C/Accession: E30538
R:Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A:Reference number: A30534; MUID:89035545; PMID:3141511
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A:Molecule type: mRNA
A:Residues: 1-112 <CLA>
A:Cross-references: UNIPARC:UPI0000176CD4
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 545; DB 2; Length 112;
Best Local Similarity 92.0%; Pred. No. 1.8e-28;
Matches 103; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60
Db 1 DIVWTGSPSSLTVSAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYGASTR 60

Qy 61 ESGVPRFTGSGSGTDFTLTISVQAEADLAIVYCCNDYSYPLTFGAGTKLEI 112
Db 61 ESGVPRFTGSGSGTDFTLTISVQAEADLAIVYCCNDHSYPLTFGAGTKLEI 112

RESULT 6
PL0264
Ig kappa chain V region (anti-DNA, D20VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: PL0264
R:Shlomchik, M.; Maecelli, M.; Shan, H.; Radic, M.Z.; Piseteky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0264
A:Molecule type: mRNA
A:Residues: 1-113 <SHL>
A:Cross-references: UNIPARC:UPI0000176AFB
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 6, 2006, 12:10:16 ; Search time 111 Seconds
(without alignments)
2402.610 Million cell updates/sec

Title: US-10-743-697-1
Perfect score: 2046
Sequence: 1 ELVWTPSPSSLVTVAGEKVT.....LDVWGCGTTLTVSSHHHHHH 378

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	666.5	32.6	262	Q65Z11_MOUSE	Q65Z11 mus musculu
2	566	27.7	243	Q7TQM2_MOUSE	Q7TQM2 mus musculu
3	528	25.8	255	Q6KX05_MOUSE	Q6KX05 mus musculu
4	527	25.8	119	Q9GYZ2_MOUSE	Q9GYZ2 mus musculu
5	524.5	25.6	617	Q4KML5_MOUSE	Q4KML5 mus musculu
6	518	25.3	487	Q65Z12_MOUSE	Q65Z12 mus sp. fy/
7	508.5	24.9	240	Q52164_MOUSE	Q52164 mus musculu
8	501.5	24.5	468	Q569W9_MOUSE	Q569W9 mus musculu
9	500	24.4	140	HV03_MOUSE	P01746 mus musculu
10	499	24.4	120	HV03_MOUSE	P01747 mus musculu
11	489.5	23.9	139	HV07_MOUSE	P01751 mus musculu
12	489	23.9	590	Q4V9V8_MOUSE	Q4V9V8 mus musculu
13	486.5	23.8	143	Q924R0_MOUSE	Q924R0 mus musculu
14	485	23.7	140	Q924P8_MOUSE	Q924P8 mus musculu
15	485	23.7	473	Q9D8L4_MOUSE	Q9D8L4 mus musculu
16	484.5	23.7	145	Q924R4_MOUSE	Q924R4 mus musculu
17	483.5	23.6	145	Q924Q7_MOUSE	Q924Q7 mus musculu
18	483	23.6	142	Q924Q1_MOUSE	Q924Q1 mus musculu
19	482.5	23.6	143	Q91V67_MOUSE	Q91V67 mus musculu
20	482	23.6	134	Q65SR6_MOUSE	Q65SR6 mus musculu
21	482	23.6	146	Q924R8_MOUSE	Q924R8 mus musculu
22	480.5	23.5	145	Q924R1_MOUSE	Q924R1 mus musculu
23	480.5	23.5	458	Q5B3Z2_RAT	Q5B3Z2 ratcus norv
24	479	23.4	114	KV4A_HUMAN	P01625 homo sapien
25	479	23.4	146	Q924Q3_MOUSE	Q924Q3 mus musculu
26	478.5	23.4	143	Q924P9_MOUSE	Q924P9 mus musculu
27	478.5	23.4	143	Q924Q5_MOUSE	Q924Q5 mus musculu
28	478	23.4	616	Q504M7_MOUSE	Q504M7 mus musculu
29	477.5	23.3	145	Q924Q6_MOUSE	Q924Q6 mus musculu
30	476	23.3	465	Q6FUB2_MOUSE	Q6FUB2 mus musculu
31	475.5	23.2	145	Q924Q9_MOUSE	Q924Q9 mus musculu

32	474.5	23.2	137	2	Q924R6_MOUSE	Q924R6 mus musculu
33	474.5	23.2	482	2	Q8K172_MOUSE	Q8K172 mus musculu
34	474	23.2	463	2	Q991C4_MOUSE	Q991C4 mus musculu
35	473	23.1	134	1	KV4C_HUMAN	P06314 homo sapien
36	472.5	23.1	464	2	Q6PF95_MOUSE	Q6PF95 mus musculu
37	472	23.1	121	1	HV01_MOUSE	P01745 mus musculu
38	472	23.1	613	2	Q8VCX7_MOUSE	Q8VCX7 mus musculu
39	471.5	23.0	145	2	Q924P7_MOUSE	Q924P7 mus musculu
40	470.5	23.0	137	1	HV11_MOUSE	P01755 mus musculu
41	470.5	23.0	141	2	Q924Q4_MOUSE	Q924Q4 mus musculu
42	470.5	23.0	145	2	Q924R3_MOUSE	Q924R3 mus musculu
43	470	23.0	140	2	Q924R2_MOUSE	Q924R2 mus musculu
44	470	23.0	470	2	Q7TQM1_MOUSE	Q7TQM1 mus musculu
45	469	22.9	144	2	Q924P5_MOUSE	Q924P5 mus musculu

ALIGNMENTS

```
RESULT 1
ID Q65Z11_MOUSE PRELIMINARY; PRT; 262 AA.
AC Q65Z11;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Anti-HIV-1 reverse transcriptase single-chain variable.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hybridoma;
RX MEDLINE=96211469; PubMed=8648670;
RA Shaheen F., Duan L., Zhu M., Bagaterra O., Pomerantz R.J.;
RT by intracellular expression of single-chain variable fragments to
RT inhibit early stages of the viral life cycle."
RL J. Virol. 70:3392-3400(1996).
DR EMBL, U48716; AAB64342.1; -; mRNA.
DR SMR, Q65Z11; 2-132.
DR GO, GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR InterPro, IPR003599; IG.
DR InterPro, IPR007110; IG-1like.
DR InterPro, IPR003598; IG_C2.
DR InterPro, IPR003596; IG_V.
DR SMART, SM00408; IG2; 2.
DR SMART, SM00406; IG1; 2.
DR PROSITE, PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; RNA-directed DNA polymerase.
SQ
SEQUENCE 262 AA; 27842 MW; 7DF20138E538E5E4 CRC64;

Query Match 32.6%; Score 666.5; DB 2; Length 262;
Best Local Similarity 48.4%; Pred. No. 6.1e-42;
Matches 132; Conservative 58; Mismatches 46; Indels 37; Gaps 7;

QY 1 ELVWTPSPSSLVTVAGEKVTMSCKSSQSLNSGNQKNTWTYQOKPGPKLIYWASTR 60
   :::::::::::::::::::::SDFLHMYQKSHSPRLIIKTAASGS 55
DB 2 DITMQSPPTLSVTPEDRVSLISCRASQST-----
QY 61 ESGVPEPRFPGSGSGTDFTLTISVAEDLAVYYCDNYSPPLTFAGTLEIK----- 113
   :::::::::::::::::::::SEVQLLESGGAEIVRPGISVAKISCAASGY 156
DB 56 IGIPERFSGSGSGDFTLSINSVPEPDGVYYCCQNGHSFPLTFAGTLEIKRADAPRT 115
   :::::::::::::::::::::
QY 114 -----GGGGGGGGGGGGGG-----SEVQLLESGGAEIVRPGISVAKISCAASGY 156
   :::::::::::::::::::::
DB 116 VSIIPPSSKLGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 174
   :::::::::::::::::::::
QY 157 APTNWLGVKVRPGHGLEWIDIPFGSGNIHYNEKFKKATLTLDKSSSTAWQSLSTLT 216
   :::::::::::::::::::::
```

Db 175 SITSGYNNWIRKFPKNDLYWGYI-NYSGDYNNPSLSKRISITADTSKNQYQLNLSVT 233
 QY 217 FEDSAVYFC-ARLNMDEPMDYWGQGTYYTSS 248
 Db 234 TEDATYYCGGGLRT---MDYWGQGTYYTSS 262

RESULT 2

07TQM2_MOUSE PRELIMINARY; PRT; 243 AA.

AC 07TQM2;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE scFv 6H8 protein (Fragment).
 GN Name=scFv 6H8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Balb/c;
 RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
 RA Peter J.C., Eftekhari P., Billiard P., Mailukat G., Hoebeke J.;
 RT "scFv single chain antibody variable fragment as inverse agonist for
 the beta-2 adrenergic receptor."
 RL J. Biol. Chem. 278:36740-36747(2003).
 DR EMBL; AJ574851; CAB00495.1; -; GenomLc_DNA.
 DR HSSP; P01751; 1A6W.
 DR 07TQM2; 1-236.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 FT NON TER 1
 SQ SEQUENCE 243 AA; 25976 MW; BEPFF64D2DCFAF76 CRC64;

Query Match 27.7%; Score 566; DB 2; Length 243;

Best Local Similarity 47.0%; Pred. No. 1.9e-34;

Matches 124; Conservative 33; Mismatches 71; Indels 36; Gaps 9;

QY 129 EVOLLESGAEVLVPGTSTVSKSCASGYAFNNYMGWVKORPGHLEWIGIPFGSGNIH 188
 Db 1 QVQLQQSGSELVPRGASVSKCSRASTFTTMMWVKQKHGQLEWIGITLYFGSGITN 59
 QY 189 YNEKFKGKATLTADKSSSTAYMOLSLTFEDSAVYFCARLRNMDEPMDYWGQGTYYVS- 247
 Db 60 YDEKFKNGILTVDTSSSTAYMHLSSLASDSAVYYCAR---GGRGLDVGAGTTLTVSS 116
 QY 248 -----SGGGSDILQOGSAGELA-RPGASVYMSCKTSGYFTTMMWVKORPGQG 297
 Db 117 GGGSGGGSGGGSDIQMTQSSSFVSGLDRVLTITKASEDIYNR--LAWYQOKRP-- 172
 QY 298 LEWIGYINPSR-----GYTNVQKFKDKATLTLDKSSSTAYMOLSLTFEDSAVYYCARYY 353
 Db 173 -----NAPRLLSGATSLSTGVPSR--FSGSGSGDYTLSTISLTQTEDAVYYICQY 223
 QY 354 DDHYCLDYWGQGTTLTVSSHHNH 377
 Db 224 STR-----TFGGGTLEIKHHNH 243

RESULT 3

06KB05_MOUSE PRELIMINARY; PRT; 255 AA.

AC 06KB05;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE scFv B8E5 protein (Fragment).
 GN Name=scFv B8E5;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Balb/c;
 RA Peter J.C., Mailukat G., Tugler J., Maurice D., Roegel J.C.,
 RA Briand J.P., Hoebeke J.;
 RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
 monoclonal anti-M2 receptor antibody fragments."
 RL J. Biol. Chem. 279:55697-55706(2004).
 DR EMBL; AJ746180; CAC34081.1; -; Other_DNA.
 DR HSSP; P01837; 1KCR.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 FT NON TER 1
 SQ SEQUENCE 255 AA; 27445 MW; B68BD3835DFF713B CRC64;

Query Match 25.8%; Score 528; DB 2; Length 255;

Best Local Similarity 90.3%; Pred. No. 1.5e-31;

Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELYMTQSPSSSLTVTAGEKVTMSCKSSQSGLNSGNQKYLWYQOKRPQPKLLIYMASTR 60
 Db 137 DIVMAQSPSSLSVAGKVKVMSCKSSQSGLNSGNQKYLWYQOKRPQSPKLLIYGASTR 196
 QY 61 ESVGPRFTSGSGGTDTLTSSVQAEADLAIVYCONDYSLPFGAGTKLEIK 113
 Db 197 ESVGPRFTSGSGGTDTLTSSVQAEADLAIVYCONDYSLPFGAGTKLEIK 249

RESULT 4

09GY22_MOUSE PRELIMINARY; PRT; 119 AA.

AC 09GY22;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-OCT-2003 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
 chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Song X.T., Feng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 variable region gene of monoclonal anti-idiotypic antibody NP30 of
 Schistosoma japonicum."
 RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF282622; AAG01452.1; -; mRNA.
 DR HSSP; P01751; 1A6W.
 DR 09GY22; 1-119.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFA6AB CRC64;

Query Match 25.8%; Score 527; DB 2; Length 119;

Best Local Similarity 78.8%; Pred. No. 6.8e-32;

Matches 93; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 255 IKLQSGAGELARPGASVYMSCKTSGYTFRTYTMWVKORPGQGLEWIGYINPSRGYNN 314
D 2 VOLVESGAEVARKPGASVYMSCKASGYTFRTYNNMVQAPGHGLEMIGYINPSRGYNN 61
QY 315 OKFEDKATLTLDKSSSTAYMQLSLTSEDSAVVYCARVDHYGLDPMWGGSTLTWSS 372
D 62 OKFADRVMTTDSFSTAYMDLRSLRSHADSAVYICARYDDHYCLDPMWGGSTLTWSS 119

RESULT 5

Q4KML5_MOUSE PRELIMINARY; PRT; 617 AA.

AC Q4KML5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;

NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marubina K., Farmer A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Cavaletto T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malik J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Wozny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC098504; AAH98504.1; -, mRNA.
KW Hypothetical protein.

SEQUENCE 617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;

Query Match

Best Local Similarity 25.6%; Score 524.5; DB 2; Length 617;
Matches 100; Conservative 9; Mismatches 13; Indels 5; Gaps 2;

QY 250 GGGSDIKLQSGAGELARPGASVYMSCKTSGYTFRTYTMWVKORPGQGLEWIGYINPSRG 309
D 16 GVHSGVQ-LQSGDELAVPGASVYMSCKASGYTFRTYNNMVQAPGHGLEMIGYINPSRG 75
QY 310 YNNYNNKFKDKATLTLDKSSSTAYMQLSLTSEDSAVVYCARVDHYGLDPMWGGSTLTWSS 365
D 76 YTKYNNKFKDKATLTLDKSSSTAYMQLSLTSEDSAVVYCAR-REGHLMLVYAMDYWGQ 134
QY 366 TLTWSS 372
D 135 TSYTVSS 141

RESULT 6

065ZL2_9MURI PRELIMINARY; PRT; 487 AA.

ID 065ZL2_9MURI
AC 065ZL2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN- ϵ tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL, S82493; AAB37424.2; -, mRNA.
DR GO, GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003598; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-sect; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG-MHC; 1.
SQ SEQUENCE 487 AA; 53578 MW; CTBAB69F30555504 CRC64;

Query Match

Best Local Similarity 25.3%; Score 518; DB 2; Length 487;
Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;

QY 125 GGGSEVOLLESGAEVARKPGASVYMSCKASGYTFRTYTMWVKORPGQGLEWIGYINPSRG 184
D 16 GVHSGVQ-LQSGDELAVPGASVYMSCKASGYTFRTYNNMVQAPGHGLEMIGYINPSRG 74
QY 185 GNIHYNEFKGKATLTLDKSSSTAYMQLSLTSEDSAVVYCARLRLNWDPMWGGSTTV 244
D 75 DDIKYNKFKGKATLTLDKSSSTAYMQLSLTSEDSAVVYFCR-----SYGHMGQGTTL 129
QY 245 TVSS-----SGGGSDIKLQSGAGELA-RPGASVYMSCKTSGYTFRTYTMWVKORP 294
D 130 TSSGGGSGGGGGGGGSRIGWTQSPASISVGLVYITCPASINISY--NLAWQOQK 187
QY 255 GGGLEWIGYIN-----PSRGYNNYNNKFKDKATLTLDKSSSTAY-MQLSLTSEDSAV 346
D 188 GSGPQLLVYATNLADGVPSR-----FSGSGSGTGYSLKINLSQSFDS 232
QY 347 YCCARYDDHYCLDPMWGGSTLTW 370
D 233 YTCQHFWGTPYR---FGGSTRLEI 253

RESULT 7

052L64_MOUSE PRELIMINARY; PRT; 240 AA.

ID 052L64_MOUSE
AC 052L64;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Db 133 TITVSSA-----KTAASVYPLAPVCGDTGGTGGVLCVKGVPPEPTLTWSSGS 183
Qy 294 PGOGLEWIGYINPGRGT 311
Db 184 LSSGVHTFPVAVLQSDLT 201

RESULT 9

HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estees P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: J00493; AAA8128.1; -, mRNA.
DR HSSB; P01747, IUPQ.
DR SMR; P01746; 20-140.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 Ig heavy chain V region 93G7.
FT DOMAIN 20 139 Ig-1like.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBEB31DASCE8 CRC64;

Query Match 24.4%; Score 500; DB 1; Length 140;
Best Local Similarity 74.8%; Pred. No. 8.9e-30;
Matches 95; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

Qy 248 SGGGSGDILQOSGAEIAPGASVSKSCSTGYTFRTYTMHWKORPGGLEWIGYINPS 307
Db 14 TAGVSHVQLQOSGAEIAPGASVSKSCSTGYTFRTYTMHWKORPGGLEWIGYINNG 73
Qy 308 RGYTNQKFKDQKATLTDDKSSSTAYMQLSLTSEDSAVYYCAR--YYDDHYCLDYWGQ 365
Db 74 NGYINNEKFKGKTTLTVDKSSSTAYMQLSLTSEDSAVYFCARSHYGGSYFDYWGQ 133

Qy 366 TITVSS 372
Db 134 TPLTVSS 140

RESULT 10
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).

RL [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-120.
RX MEDLINE=21528949; PubMed=11673524;
RA Parham-Seren B., Viswanathan M., Strong R.K., Margolies M.N.;
RT "Structural analysis of mutants of high-affinity and low-affinity p-
RT azophenylarsenate-specific antibodies generated by alanine scanning of
RT heavy chain complementarity-determining region 2."
RL J. Immunol. 167:5129-5135(2001).
CC -1- MISCELLANEOUS: From analysis of the sizes of several other
CC differentiated genes that hybridize to this one, the authors
CC conclude that all of these V regions have rearranged to the same J
CC segment, JH2.

CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR PIR; A94264; HVMG7.
DR PDB; IUPQ; X-ray; H=1-120.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM 3D-structure; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 111 Ig-1like.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04EA4167B654AF CRC64;

Query Match 24.4%; Score 499; DB 1; Length 120;
Best Local Similarity 78.3%; Pred. No. 8.7e-30;
Matches 94; Conservative 7; Mismatches 17; Indels 2; Gaps 1;

Qy 255 IYLOOSGAEIAPGASVSKSCSTGYTFRTYTMHWKORPGGLEWIGYINSGYTN 314
Db 1 VOLQOSGAEIAPGASVSKSCSTGYTFRTYTMHWKORPGGLEWIGYINSGTXXN 60
Qy 315 OKFKQKATLTDDKSSSTAYMQLSLTSEDSAVYYCAR--YYDDHYCLDYWGQ 372
Db 61 EKFKGKTTLTVDKSSSTAYMQLSLTSEDSAVYFCARSHYGGSYFDYWGQ 120

RESULT 11
HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234546; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RA "heavy chain variable region contribution to the NpB family of RT antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
 CC -1- MUSELANE005: The Bl-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl (NpB antibodies).
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL, J00529, AAA38170.1, -, mRNA.
 DR PIR, A90809, MHMS18.
 DR PDB, 1A6U; X-ray; H=20-139.
 DR PDB, 1A6V; X-ray; H/I/J=20-139.
 DR PDB, 1A6W; X-ray; H=20-139.
 DR PDB, 1NGP; X-ray; H=20-139.
 DR PDB, 1NGQ; X-ray; H=20-139.
 DR PDB, 1NOB; X-ray; A/C=20-139.
 DR Ensemble; ENSMUSG0000063737; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 139 Ig heavy chain V region Bl-8/186-2.
 FT REGION 20 49 Framework-1.
 FT REGION 50 54 Complementarity-determining-1.
 FT REGION 55 68 Framework-2.
 FT REGION 69 85 Complementarity-determining-2.
 FT REGION 86 117 Framework-3.
 FT REGION 118 124 D segment.
 FT REGION 125 139 JH2 segment.
 FT DISUFID 41 115 By similarity.
 FT NON_TER 139 139
 FT STRAND 22 24
 FT STRAND 28 31
 FT TURIN 33 34
 FT STRAND 37 44
 FT HELIX 48 50
 FT STRAND 52 58
 FT TURIN 60 61
 FT STRAND 64 70
 FT TURIN 72 74
 FT STRAND 77 79
 FT HELIX 81 83
 FT TURIN 84 86
 FT STRAND 87 92
 FT TURIN 93 96
 FT STRAND 97 102
 FT HELIX 107 109
 FT STRAND 111 118
 FT TURIN 120 123
 FT STRAND 129 129
 FT STRAND 133 137
 SO SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
 Query Match 23.9%; Score 489.5; DB 1; Length 139;
 Best Local Similarity 72.0%; Pred. No. 5.4e-29;
 Matches 95; Conservative 12; Mismatches 20; Indels 5; Gaps 2;

QY 244 VTWSGGGSGDILKQSGAEIAPGASVXNSCTSGYTRTYMHWKORPGGLEWIGY 303
 Db 10 LAATATGVHSQVQLQPGAEIVKPGASVKRSCASGYFTSYMMHWKQSPGRLIEWIGR 69
 QY 304 INPSRGYTNQKFKDKATITTDKSSSTAYMQLSSLTSESAVYTCARYDDHY---CLD 360
 Db 70 IDNSGGTXXNEKFKKATLTVDKPSSTAYMQLSSLTSESAVYTCARY--DYVGSAYFD 127
 QY 361 YMGQGTTLTVSS 372
 Db 128 YMGQGTTLTVSS 139
 RESULT 12
 Q4V9V8_MOUSE
 ID Q4V9V8_MOUSE PRELIMINARY; PRT; 590 AA.
 AC Q4V9V8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN Name=Igh-6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Saplenton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Udell T.B., Tohiyuki S., Casarini P., Prange C., Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalene D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary gland;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC096667; AA95667.1, -, mRNA.
 DR MGI; MGI:96448; Igh-6.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig CL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IGV.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00409; IG 2.
 DR SMART; SM00407; IGC1; 4.
 DR SMART; SM00406; IGV 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SO SEQUENCE 590 AA; 64892 MW; D42518F9A188B14 CRC64;
 Query Match 23.9%; Score 489; DB 2; Length 590;

Oy		122	GSGGGGSEVLLLEGGAEIVPPTGSVKISCSAGYAFNTNVLGMWKORPHGIEWIDIF	181
Dd		13	GTAGVHCQVQ-LKOSGAELVRPGASVKLSCASGYTFPDYYINWVKORPGGLEWIARIY	71
Oy		182	PGSGNIHNENPKGATLTITADKSSSTAYMOISSLFEEDSAVFCAFLNNDEPMVMYGOG	241
Dd		72	PGSGNTTYNEPKGATLTIAEKSSSTAYMOLSLTSDSAVFFCAFT--GTGMIDYMGOG	128
Oy		242	TTVTYVS 248	
Dd		129	TSVTYVS 135	
 RESULT 13 O924R0_MOUSE PRELIMINARY; PRT, 143 AA.				
ID	O924R0_MOUSE	PRT,	143	AA.
AC	O924R0_			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DR	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	VH186.2-D-J-C mu protein (Fragment).			
CN	Name=VH186.2-D-J-C mu;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OX	Muridae; Murinae; Mus.			
RN	NCBI_TaxID=10090;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Kozono Y., Kozono H., Azuma T.;			
RC	STRAIN=C57BL/6;			
RL	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.			
RP	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Corbet S., Hitt M., Roth C., Theze J., Fougereau M., Schif C.;			
RT	"Allogeneic manipulation of the GAP idiotypic cascade. Immunization of			
RT	C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-			
RT	specific V genes as the original antigen.";			
RL	J. Immunol. 141:779-784(1988).			
RN	(3)			
RP	NUCLEOTIDE SEQUENCE.			
RA	Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;			
RT	"Two murine natural polyreactive autoantibodies are encoded by			
RT	nucleated germ-line genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).			
DR	EMBL; AB067790; BAB63275.1; -, mRNA.			
DR	PIR; F28833; F28833.			
DR	PIR; F33932; F33932.			
DR	PIR; PH105; PH105.			
DR	PIR; PH108; PH108.			
DR	PIR; PH114; PH114.			
DR	PIR; PH118; PH118.			
DR	PIR; PH119; PH119.			
DR	PIR; PH125; PH125.			
DR	PIR; PH126; PH126.			
DR	PIR; PH128; PH128.			
DR	PIR; PH129; PH129.			
DR	PIR; PH131; PH131.			
DR	PIR; PH134; PH134.			
DR	PIR; PH137; PH137.			
DR	PIR; PH139; PH139.			
DR	PIR; PH142; PH142.			
DR	PIR; PH144; PH144.			
DR	PIR; PH147; PH147.			
DR	PIR; PH149; PH149.			
DR	PIR; PH150; PH150.			
DR	PIR; PH151; PH151.			
DR	PIR; PH152; PH152.			

```

DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMR; O924P8; 1-134.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
FT NON_TER
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match 23.8%; Score 486.5; DB 2; Length 143;
Best Local Similarity 76.3%; Pred. No. 9.4e-29;
Matches 90; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

Qy 255 IKLOQSGAEIARPGASVYKMSCKTSGYTFRTYTMHVMKORPGQGLEWIGYINPSRGYTNV 314
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VOLQDQGEIYKPGASVYLSCKASGYFTSYWMHVMKORPGKLEWIGRIDPNNGGTTCN 61

Qy 315 QKFKKATILTTDKSSSTAYMQLSSLTSEDSAVVYCARYYDDHYCLDYWGQGTTLTVSS 372
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 EKFSKATILTYDKSSSTAYMQLSSLTSEDSAVVYCAR-WBDDYMDVYGQGTSTVSS 118

RESULT 14
Q924P8_MOUSE PRELIMINARY; PRT; 140 AA.
ID Q924P8_MOUSE PRELIMINARY;
AC Q924P8;
DT 01-DEC-2001 (TREMBLrel. 19; Created)
DT 01-DEC-2001 (TREMBLrel. 19; Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN Name=AB069917; Synonyms=V23-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN RN
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbett S., Hirt M., Roth C., Theze J., Fougereau M., Schmitt C.;
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific v genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL; AB069917; BAB65933.1; -, mRNA.
DR PIR; 128833; 128833.
DR HSSP; P01751; 1A6W.
DR SMR; Q924P8; 1-126.
DR WGI; WGI:3576502; AB069917.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
FT NON_TER
SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;

Query Match 23.7%; Score 485; DB 2; Length 140;
Best Local Similarity 78.8%; Pred. No. 1.2e-28;
Matches 93; Conservative 6; Mismatches 15; Indels 4; Gaps 1

Qy 255 IKLOQSGAEIARPGASVYKMSCKTSGYTFRTYTMHVMKORPGQGLEWIGYINPSRGYTNV 314
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VOLQDQGEIYKPGASVYLSCKASGYFTSYWMHVMKORPGKLEWIGRIDPNNGGTTCN 61

```

QY 315 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYCAFYVDHXCCLDYGQGTTLTVSS 372
 Db 62 EKFKSKATLTVDKSSSTACQSLTSEDSAVYCAFNWD----FDYMGQGTTLTVSS 115

RESULT 15
 ID Q9DBL4 MOUSE PRELIMINARY; PRT; 473 AA.
 AC Q9DBL4;
 DT 01-JUN-2001 (TrEMBL:rel. 17, Created)
 DT 01-JUN-2001 (TrEMBL:rel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBL:rel. 26, Last annotation update)
 DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
 DE library, clone:181060009 product:immunoglobulin heavy chain 6 (heavy
 DE chain of IgM), full insert sequence.
 GN Name=Igh-1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,
 RA Akawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakaido I., Pesole G., Quackenbush J.,
 RA Kuhl L.M., Srauli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicchi S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momtaz P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RL [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RL [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Tameda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RL [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RL [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,
 RA Akawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakaido I., Pesole G., Quackenbush J.,
 RA Kuhl L.M., Srauli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicchi S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momtaz P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RL [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [9]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Query Match 23.7%; Score 485; DB 2; Length 473;
 Best Local Similarity 50.2%; Pred. No. 5.3e-28;
 Matches 109; Conservative 20; Mismatches 56; Indels 32; Gaps 4;

QY 123 SGGGSEVQLLESGAEIVRPGTSVKISCAAGATNTNVLGVNKPFGHLEWIDIFP 182
 Db 14 TAGVHCQVQ-LKOSGAEIVRPGTSVKISCAAGATNTNVLGVNKPFGHLEWIDIFP 72
 QY 183 GSGNIHNEKFKATLTTADKSSSTAYMQLSSLTSEDSAVYFCARLRNWDPMYMGQT 242
 Db 73 GSGSTYNEKFKATLTTADKSSSTAYMQLSSLTSEDSAVYFCARLSYDWDPMYMGQT 132
 QY 243 TVTVSSGG-----GGSIDIKLQSGAEIVRPGTSVKISCAAGATNTNVLGVNKPFGHLEWIDIFP 289

Db 133 LVTISA AKTAPSVYPLAPVCGI-----TGSSVTUGCLVKGYFPEPVITW 179
QY 290 VKORPGGLEWIGYINPSRGYTNYNQKFKDKATLITD 326
Db 180 NSGSLSSGVHTFPALOGGLYT-----LSSSVTVTSN 211

Search completed: March 6, 2006, 14:48:20
job time : 113 secs

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Qy	Db
280 YVTRATVTHMVKKORPGQGLEMIIGYNISPGYNNYKQKFDKATLTTPDSSSTAYMOSSL	313 YASRSMNMMVWVKORPGQGLEMIIGRITPGQGDITNNYKGRKGRATLTLPDSSSTAYMOYSSL
340 TSEDSAVYYICAR--YTDHGYCLDYMGGGTTLVSS	373 TSVDASAIFYFCARGNTVVVPEYMDYMGQGTTLVSS

RESULT 2
US-11-116-939-11

```

1 Sequence ID: US/11/116939
2 Publication No. US20050265995A1
3 GENERAL INFORMATION:
4 APPLICANT: Stephen Tomlinson
5 APPLICANT: Richard J. Oligg
6 TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
7 FILE REFERENCE: 19113.0115U2
8 CURRENT APPLICATION NUMBER: US/11/116,939
9 CURRENT FILING DATE: 2005-04-28
10 PRIOR APPLICATION NUMBER: 60/565,907
11 PRIOR FILING DATE: 2004-04-28
12 NUMBER OF SEQ ID NOS: 27
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 11
15 LENGTH: 824
16 TYPE: PRT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
20 OTHER INFORMATION: construct
21 US-11-116-939-11

```

Query Match	48.5%	Score	992.5	DB	7	Length	824
Best Local Similarity	61.8%	Pred. No.	1.4e-55				
Matches	204	Conservative	26	Mismatches	53	Indels	47
						Gaps	6

```

Oy      1 ELVWTOSSPSLTVTAGEKVTMCSKSSQSLNNGNOKNYLTWYQOKPQOPPTLLIYMASTR 60
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      25 DYMSQSPSSLAVSVEKTMCKSSQSL--KTNOKNYIATYQXKPGQSPDLLIYMASSR 82
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      61 ESGVPDRFTSGSGGTDFTLLISSLVQAEDLAVYYCONDYSLPTFGAGTKLEIKGGGGSGG 120
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      83 ESGVPDRFTSGSGGTDFTLLISSLVKAEDLAVYYCQOQYSSPLTFAGATKLEIKGGGGSGG 142
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      121 GSGGGGG-----SIVQLLESGAEIYPRGTIVKISCSASGATPTNY 161
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      143 GGSQGGGSGMCMSCVMLFVATATGVHSQVO--LEQSGPELVKRGYSVKISCKSGSGTFTDY 201
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      162 WIAGVKORPGHGLEWIGDIFPGSGNIHYNEKFKGATLTADSSSTAWMQSLSTFEDSA 221
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      202 AIHHVKSQSHAKSLFEMIGIVSTYYGHHYHQQKRGKRLTLVDSNSTATAMELARLTSEBSA 261
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      222 VYFCARLRNWD-----PMDYWGQFTTVTVSSGGGGSDIKLQOQSGAEIARP----- 267
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      262 IYVCARPNNNYSSPPYAMDQMGQSTVTVSSGGGGSGGGSGGSCPAPLPFYAKPI 321
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      268 -----GASVYKMSCKTSGTFTFRITM 287
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      322 NPDTDSFTFWGTSLSKTECR--PGYIKQOFISI 350
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 3
US-11-116-939-12
Sequence 12, Application US/11116939
Publication No. US20050265995A1
GENERAL INFORMATION:
APPLICANT: Stephen Tomlinson
APPLICANT: Richard J. Oulgg
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
FILE REFERENCE: 19113.011502
CURRENT APPLICATION NUMBER: US/11/116,939

```

: CURRENT FILING DATE: 2005-04-28
: PRIOR APPLICATION NUMBER: 60/566,907
: PRIOR FILING DATE: 2004-04-28
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
: LENGTH: 412
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
: OTHER INFORMATION: construct
: OS-11-116-939-12

```

Query Match	Score	DB	Length
48.5%	992	7	412

Matches 203; Conservative 24; Mismatches 41; Indels 42; Gaps 6;

```

QY      1 ELVMTDSPESLIVTAGEKWTMSCKSSGSLNSGNQKYLITWYQOKPEQPKELIYNASTR 60
Db      25 DIYMSGSPESLIVSAGEKWTMSCKSSGSL- KTMQKYLITWYQOKPEQSSFKLLIYNAASR 82

QY      61 ESGVDPFRFGSGSGGTDFTLLTISVQAEDLAVYYCONDYSPYLFAGATKLELNGGSGSG 120
Db      83 ESGVDPFRFTGSSGSGDFTLLTISVQAEDLAVYYQYQYSPYLFAGATKLELNGGSGSG 142

QY      121 GSGGGG-----SEVQLLREQSGAEIVRPGTSVKISCKASGAFATNY 161
Db      143 GSGGGGSGMGSCWMLFLVATATGVHSGVQ-LEQSGPELVRPGVSVKISCKSGGYFTDY 201

QY      162 WLCAWYKQRPQHGLEWLEIGDIPFQSGNIHNEKFKGKATILTADKSSSTAYMOLSLTFEDSA 221
Db      202 AITMYVQSHAKSLLEWIGVISTYGGTHNQCFKKAKATILTVDKSSNTIYMEELATLSDDS 261

QY      222 VYFCALALRWDE-----FMDYWGCGTTLTVSSGGGSGSDIKLQSGAEALRPGAIVK----- 272
Db      262 IYYCAPNNYSGSPRYAMDGCGQSTVTVSSGGG-----SGGGSGSGGSGSLRCYNC 314

QY      273 ---MSCKT 278
Db      315 LDPVSSCKTN 324

```

RESULT 4

```

US-11-116-939-10
Sequence 10, Application US/1116939
Publication No. US20050265995A1
GENERAL INFORMATION:
APPLICANT: Stephen Tomlinson
APPLICANT: Richard J. Quigg
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
FILE REFERENCE: 19113.0115U2
CURRENT APPLICATION NUMBER: US/11/116,939
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 60/565,907
PRIOR FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 293
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
US-11-116-939-10

```

[illegible]

```
Db 25 DVMGSPSSSLAVSGEKTVMNCKSSQSL--KTNNKYIYLAHYQKPGQSPKLLIYMASTR 82
Qy 61 ESGVDRFTSGSGTDFLTLTISVQAEADLAVYYCONDYSPYLPFGAGTKLEIKGGGSGG 120
Db 83 ESGVDRFTSGSGTDFLTLTISVQAEADLAVYYCONDYSPYLPFGAGTKLEIKGGGSGG 142
Qy 121 GSGGGG-----SEVQLLESGAEIVRPGTSVKISCAAGYAFTNY 161
Db 143 GSGGGGSGMGWCVMLFLVATATGVHSQVQ--LEQSGPELVAPGVSVKISCKSGGTYFTDY 201
Qy 162 WLGVKQRPQHGLEMIGDIPFGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSTLPEDSA 221
Db 202 AIHWKQSHAKSLMIGVISTYGHYNNQKFKGKATLTADKSSSTAYMQLSSTLPEDSA 261
Qy 222 VYFCARLRNMD-----PMDYMGQGTITVYSS 248
Db 262 IYCARPRNNYSSPPYYAMDGMGQGTISVYSS 293

RESULT 5
US-10-981-356A-29
; Sequence 29, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 29
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-29

Query Match 46.5%; Score 952; DB 6; Length 666;
Best Local Similarity 55.4%; Pred. No. 4.2e-53;
Matches 209; Conservative 36; Mismatches 86; Indels 46; Gaps 10;

Qy 1 ELVMTQSPSSLTLYVAGEKVTMSCKSSQSLNSGNQKNTLYVQKRGQPKLLIYMASTR 60
Db 1 DIMMTQSPSSSLAVSAGEKVTMSCKSSQSLVYSSNKNYLAHYQKPGQSPKLLIYMASTR 60
Qy 61 ESGVDRFTSGSGTDFLTLTISVQAEADLAVYYCONDYSPYLPFGAGTKLEIKGGGSGG 120
Db 61 ESGVDRFTSGSGTDFLTLTISVQAEADLAVYYCONDYSPYLPFGAGTKLEIKGGGSGG 112
Qy 121 GSGGGGSEVQLLESGAEIVRPGTSVKISCAAGYAFTNYWLGVKQRPQHGLEMIGDI 180
Db 113 --RTVAAPSVFIFPPSDEQL-KSGT-A-SVVC-----LNNFYPRAK-----VGMKVDN 157
Qy 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSTLPEDSAVYFCARLRNMDDEPM 235
Db 158 ALQSGN-----SQESVTEQDSKDYSLSTLTLSKADYEKHKVYAC-----EV 201
Qy 236 DVMGQGTITVYSSGSGGSDIKLQSGAEILAPGASVYMSCKTSGYTFRTYTMHWKQRP 295
Db 202 THQGLSSPYTKSFNNGECEEVQLQSGAEIVRPGTSVKISCAAGYAFTNYLIEWKQRP 261
Qy 296 QGLEWIGYINPGRGYTNYNQKFKGKATLTADKSSSTAYMQLSSTLPEDSAVYFCARYDD 355
Db 262 QGLEWIGVNNPGRGGSNNYNEKFKGKATLTADKSSSTAYMQLSSTLPEDSAVYFCAR--SG 319
Qy 356 HYCLDYGQGTITVYSS 372
Db 320 GFYFDYMGQGTISVYSS 336
```

```
RESULT 6
US-11-096-046-29
; Sequence 29, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-29

Query Match 46.1%; Score 942.5; DB 7; Length 667;
Best Local Similarity 55.3%; Pred. No. 1.7e-52;
Matches 209; Conservative 37; Mismatches 85; Indels 47; Gaps 11;

Qy 1 ELVMTQSPSSLTLYVAGEKVTMSCKSSQSLNSGNQKNTLYVQKRGQPKLLIYMASTR 60
Db 1 DIMMTQSPSSSLAVSAGEKVTMSCKSSQSLVYSSNKNYLAHYQKPGQSPKLLIYMASTR 60
Qy 61 ESGVDRFTSGSGTDFLTLTISVQAEADLAVYYCONDYSPYLPFGAGTKLEIKGGGSGG 120
Db 61 ESGVDRFTSGSGTDFLTLTISVQAEADLAVYYCONDYSPYLPFGAGTKLEIKGGGSGG 112
Qy 121 GSGGGGSEVQLLESGAEIVRPGTSVKISCAAGYAFTNYWLGVKQRPQHGLEMIGDI 180
Db 113 --RTVAAPSVFIFPPSDEQL-KSGT-A-SVVC-----LNNFYPRAK-----VGMKVDN 157
Qy 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSTLPEDSAVYFCARLRNMDDEPM 235
Db 158 ALQSGN-----SQESVTEQDSKDYSLSTLTLSKADYEKHKVYAC-----EV 201
Qy 236 DVMGQGTITVYSS--SGGGSDIKLQSGAEILAPGASVYMSCKTSGYTFRTYTMHWKQRP 294
Db 202 THQGLSSPYTKSFNNGECEEVQLQSGAEIVRPGTSVKISCAAGYAFTNYLIEWKQRP 261
Qy 296 QGLEWIGYINPGRGYTNYNQKFKGKATLTADKSSSTAYMQLSSTLPEDSAVYFCARYDD 354
Db 262 QGLEWIGVNNPGRGGSNNYNEKFKGKATLTADKSSSTAYMQLSSTLPEDSAVYFCAR--S 319
Qy 355 DHYCLDYGQGTITVYSS 372
Db 320 GFYFDYMGQGTISVYSS 337
```

```
RESULT 7
US-11-084-717-21
; Sequence 21, Application US/11084717
; Publication No. US20050260736A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI-JUN
; APPLICANT: HARVEY, BARRETT R.
```


Db 234 MDYMGQGTSTVTSS 247

RESULT 10
US-11-084-717-23

/ Sequence 23, Application US/11084717
/ Publication No. US20050260736A1
/ GENERAL INFORMATION:
/ APPLICANT: GEORGIOU, GEORGE
/ APPLICANT: JEONG, KI-JUN
/ APPLICANT: HARVEY, BARRETT R.
/ APPLICANT: IVERSON, BRENT L.
/ TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
/ FILE REFERENCE: UTSA:723US
/ CURRENT APPLICATION NUMBER: US/11/084,717
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: 60/554,324
/ PRIOR FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: 10/620,278
/ PRIOR FILING DATE: 2003-07-15
/ PRIOR APPLICATION NUMBER: 60/396,058
/ PRIOR FILING DATE: 2002-07-15
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
US-11-084-717-23

Query Match 40.6%; Score 830.5; DB 7; Length 247;
Best Local Similarity 63.4%; Pred. No. 7.7e-46; Indels 13; Gaps 3;
Matches 161; Conservative 33; Mismatches 47;

QY 1 ELVMTGSPSSLTVAAGEKVTMSCKSSQSLNSGNKNTLWYQKPGQPPKLLIYMASTR 60
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 DIQMTQTSSLSASLGDRTVSCRASQDI-----RNYLWYQKPGQPPKLLIYTSRL 54
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 ESGVDRFTSGSGTDFLTITSSVQAEPLAVYQNDYSYPLTFGAGTKLEIK-----G 114
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 55 QGVPSRFSGSGGSDYSLTINLEQEDIGTYFCQCGNTPTWTFGGTKLEIKRGGGSGSD 114
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 115 GGGSGGGSGGGSEVOQLQSGAEIVRPGTSVKISCKASGAFNNWLGWVKORPGHGL 174
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 115 GGGSGGGSGGGSEVOQLQSGPELVKPGASVKISCKDSGAFNWSMNNWVKORPGQGL 173
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 175 EMIGDIFPGSGNIHNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDP 234
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 174 EMIGRIYGDSDSNNGKFEKALITADKSSSTAYMQLSLTSVDSAVYFCARSGLLRYA 233
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 235 MDYMGQGTSTVTSS 248
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 234 MDYMGQGTSTVTSS 247
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
US-11-179-244-23

/ Sequence 23, Application US/11179244
/ Publication No. US20050267294A1
/ GENERAL INFORMATION:
/ APPLICANT: HARVEY, BARRETT R.
/ APPLICANT: GEORGIOU, GEORGE
/ APPLICANT: IVERSON, BRENT L.
/ TITLE OF INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS
/ FILE REFERENCE: UTSA:721US
/ CURRENT APPLICATION NUMBER: US/11/179,244
/ CURRENT FILING DATE: 2005-07-12
/ PRIOR APPLICATION NUMBER: US/10/620,049
/ PRIOR FILING DATE: 2003-07-15

/ PRIOR APPLICATION NUMBER: 60/396,058
/ PRIOR FILING DATE: 2002-07-15
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-179-244-23

Query Match 40.6%; Score 830.5; DB 7; Length 247;
Best Local Similarity 63.4%; Pred. No. 7.7e-46; Indels 13; Gaps 3;
Matches 161; Conservative 33; Mismatches 47;

QY 1 ELVMTGSPSSLTVAAGEKVTMSCKSSQSLNSGNKNTLWYQKPGQPPKLLIYMASTR 60
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 DIQMTQTSSLSASLGDRTVSCRASQDI-----RNYLWYQKPGQPPKLLIYTSRL 54
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 ESGVDRFTSGSGTDFLTITSSVQAEPLAVYQNDYSYPLTFGAGTKLEIK-----G 114
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 55 QGVPSRFSGSGGSDYSLTINLEQEDIGTYFCQCGNTPTWTFGGTKLEIKRGGGSGSD 114
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 115 GGGSGGGSGGGSEVOQLQSGAEIVRPGTSVKISCKASGAFNNWLGWVKORPGHGL 174
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 115 GGGSGGGSGGGSEVOQLQSGPELVKPGASVKISCKDSGAFNWSMNNWVKORPGQGL 173
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 175 EMIGDIFPGSGNIHNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDP 234
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 174 EMIGRIYGDSDSNNGKFEKALITADKSSSTAYMQLSLTSVDSAVYFCARSGLLRYA 233
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 235 MDYMGQGTSTVTSS 248
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 234 MDYMGQGTSTVTSS 247
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
US-11-084-055B-23

/ Sequence 23, Application US/11084055B
/ Publication No. US20060029947A1
/ GENERAL INFORMATION:
/ APPLICANT: GEORGIOU, GEORGE
/ APPLICANT: JEONG, KI JUN
/ APPLICANT: IVERSON, BRENT L.
/ TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING BY
/ FILE REFERENCE: UTSA:722US
/ CURRENT APPLICATION NUMBER: US/11/084,055B
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: 60/554,260
/ PRIOR FILING DATE: 2004-03-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
US-11-084-055B-23

Query Match 40.6%; Score 830.5; DB 7; Length 247;
Best Local Similarity 63.4%; Pred. No. 7.7e-46; Indels 13; Gaps 3;
Matches 161; Conservative 33; Mismatches 47;

QY 1 ELVMTGSPSSLTVAAGEKVTMSCKSSQSLNSGNKNTLWYQKPGQPPKLLIYMASTR 60
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 DIQMTQTSSLSASLGDRTVSCRASQDI-----RNYLWYQKPGQPPKLLIYTSRL 54
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 ESGVDRFTSGSGTDFLTITSSVQAEPLAVYQNDYSYPLTFGAGTKLEIK-----G 114
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OTHER INFORMATION: Peptide
US-11-084-0558-25

Query Match 40.3%; Score 825.5; DB 7; Length 247;
Best Local Similarity 63.4%; Pred. No. 1.6e-45;
Matches 161; Conservative 32; Mismatches 48; Indels 13; Gaps 3;

Qy	1	ELVMTOSPSLVTAGEKVTWSCKSSQSLNNGNQKNTLWYQOKPGQPPKLLIYWASTR	60
Db	1	DIQMTQTSSLSASLGDRTVSCRASQDI-----RNYLWYQOKPDGTVEFLIYTSRL	54
Qy	61	ESGVPRFTSGSGTDFTLTSSVOAEDLAVYICNDYSPYPLTFGAGTKLEIK-----G	114
Db	55	LPGVPSRFRSGSGGTDYSLITINMLEQEDIGTYFCQGNTPPWTFGGTKLEIKGGGGSD	114
Qy	115	GGSGGGGGGGGGSEVOLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKORPGHGL	174
Db	115	GGSGGGGGGGGGSEVQ-LQSGPELVKPGASVKISCKDSGYAFNSMNMWVKORPGQGL	173
Qy	175	EWIGDIPFGSGNIHYNEKFKGKATLTADKSSSTAYMOLSLTFEDSAVYFCARLRNMDEP	234
Db	174	EWIGRIYFGDDSNYNGKFEKGKILTTADKSSSTAYMOLSLTSVDSAVYFCARSGLRVA	233
Qy	235	MDYMGQGTFTTVSS	248
Db	234	MDYMGQGTSTTVSS	247

Search completed: March 6, 2006, 13:22:29
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: March 6, 2006, 13:19:02 ; Search time 80 Seconds
(without alignments)
1974.244 Million cell updates/sec

Title: US-10-743-697-1

Perfect score: 2046
Sequence: 1 ELVMTQSPSSLTVTAGEKVT.....LDYWGQGTTLTVSSHHHHH 378

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.rep:.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.rep:.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.rep:.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.rep:.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.rep:.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.rep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2046	100.0	378	5	US-10-743-697-1
2	1484.5	72.6	495	3	US-09-948-004-18
3	1484.5	72.6	495	5	US-10-672-932-18
4	1467	71.7	500	4	US-10-168-809-22
5	1439.5	70.4	499	5	US-10-805-177-111
6	1414	69.1	492	4	US-10-682-845-59
7	1409	68.9	492	4	US-10-682-845-61
8	1407	68.8	492	4	US-10-682-845-87
9	1406	68.7	492	4	US-10-682-845-65
10	1406	68.7	492	4	US-10-682-845-67
11	1405	68.7	492	4	US-10-682-845-63
12	1405	68.7	492	4	US-10-682-845-71
13	1404	68.6	492	4	US-10-682-845-69
14	1401	68.5	492	4	US-10-682-845-73
15	1401	68.5	492	4	US-10-682-845-85
16	1399	68.4	492	4	US-10-682-845-77
17	1397	68.3	492	4	US-10-682-845-75
18	1397	68.3	492	4	US-10-682-845-83
19	1395	68.2	492	4	US-10-682-845-79
20	1390	67.9	492	4	US-10-682-845-81
21	1326.5	64.8	524	5	US-10-805-177-113
22	1305	63.8	532	6	US-11-036-098-18
23	1289	63.0	507	4	US-10-239-656-47
24	1189.5	58.1	895	4	US-10-296-085A-17
25	1189.5	58.1	895	4	US-10-296-085A-27
26	1189.5	58.1	895	5	US-10-496-179-4
27	1189.5	58.1	896	4	US-10-296-085A-17

28	1189.5	58.1	896	4	US-10-296-085A-26	Sequence 26, Appl
29	1189.5	58.1	896	5	US-10-496-179-2	Sequence 2, Appl
30	1189.5	58.1	895	5	US-10-496-179-7	Sequence 7, Appl
31	1189.5	58.1	899	4	US-10-296-085A-28	Sequence 28, Appl
32	1189.5	58.1	899	5	US-10-496-179-5	Sequence 5, Appl
33	1186.5	58.0	895	4	US-10-296-085A-20	Sequence 20, Appl
34	1186.5	58.0	896	4	US-10-296-085A-18	Sequence 18, Appl
35	1186.5	58.0	896	5	US-10-496-179-3	Sequence 3, Appl
36	1138.5	55.6	510	4	US-10-239-656-49	Sequence 49, Appl
37	1135.5	55.5	510	4	US-10-239-656-79	Sequence 79, Appl
38	1131.5	55.3	503	4	US-10-239-656-75	Sequence 75, Appl
39	1128.5	55.2	499	4	US-10-239-656-73	Sequence 73, Appl
40	1124.5	55.0	499	4	US-10-239-656-77	Sequence 77, Appl
41	1087	53.1	503	4	US-10-239-656-77	Sequence 350, App
42	1070.5	52.3	768	4	US-10-627-556-115	Sequence 115, App
43	1070.5	52.3	768	5	US-10-634-862-11	Sequence 11, Appl
44	955	46.7	456	4	US-10-987-454-221	Sequence 221, App
45	954	46.6	562	5	US-10-987-454-221	

ALIGNMENTS

```
RESULT 1
US-10-743-697-1
Sequence 1, Application US/10743697
Publicatation No. US20050136050A1
GENERAL INFORMATION:
APPLICANT: KUFER, PETER
APPLICANT: BERRY, MERRY
APPLICANT: BAUELERLE, PATRICK
APPLICANT: ITIN, CHRISTIAN
TITLE OF INVENTION: BISPECTIFIC ANTIBODIES
FILE REFERENCE: DEBB:02805
CURRENT APPLICATION NUMBER: US/10/743,697
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-743-697-1
Query Match 100.0%; Score 2046; DB 5; Length 378;
Best Local Similarity 100.0%; Pred. No. 9.9e-129;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELVMTQSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNTYTWQKRGQPPKLLIYASTR 60
DB 1 ELVMTQSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNTYTWQKRGQPPKLLIYASTR 60
QY 61 EGVGPDRTFGSSGSDFTLTSSVQAEDLAIVYVCONVYPLTFPGGTLEIKGGGSGG 120
DB 61 EGVGPDRTFGSSGSDFTLTSSVQAEDLAIVYVCONVYPLTFPGGTLEIKGGGSGG 120
QY 121 GSGGGGSGSVQLLESGAEIVRPGTSVKISCKASGAFNTYMLGWKQKRGHLEWIGDI 180
DB 121 GSGGGGSGSVQLLESGAEIVRPGTSVKISCKASGAFNTYMLGWKQKRGHLEWIGDI 180
QY 181 PFGSGNIHNEKFKGATLTADKSSSTAYMQLSLTFEDSAVYFCARLKNWDEPMYWGQ 240
DB 181 PFGSGNIHNEKFKGATLTADKSSSTAYMQLSLTFEDSAVYFCARLKNWDEPMYWGQ 240
QY 241 GTTYVSSGGGSDIKLQSGAEIARPGASVMSCKTSQYTFRTYTMHWKORPGGLEW 300
DB 241 GTTYVSSGGGSDIKLQSGAEIARPGASVMSCKTSQYTFRTYTMHWKORPGGLEW 300
QY 301 IGYNPSRYTYNNQFKDKATLTDDKSSSTAYMQLSLTFEDSAVYCARYYDDHYCLD 360
DB 301 IGYNPSRYTYNNQFKDKATLTDDKSSSTAYMQLSLTFEDSAVYCARYYDDHYCLD 360
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Db 301 IGYINPBGYNTYNQKFKDRAKATLTTDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 360
Qy 361 YMGQGTTLTVSSHHHHH 378
Db 361 YMGQGTTLTVSSHHHHH 378

RESULT 2
US-09-948-004-18
; Sequence 18, Application US/09948004
; Publication No. US20030017979A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matchias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-18

Query Match 72.6%; Score 1484.5; DB 3; Length 495;
Best Local Similarity 74.7%; Pred. No. 4.2e-91;
Matches 278; Conservative 34; Mismatches 53; Indels 7; Gaps 2;

Qy 1 ELVMTGSSSLTVTAGEKVTMSCKSSQSLNSGNQKYLTVYQKPGQPPKLLIYMASTR 60
Db 1 DIVLTGSPASLASVGETVITTCRASENIY-----SYLAWYQKQKSPQLLYNAKTL 54
Qy 61 ESGVPRFTSGSGGTDTLTISSVQAEPLAVYVCOMDYSPYLTGAGTKLEIKGGGSGG 120
Db 55 TBGVPSRFGSGSGGTQSLKINSLOPEDFGNYFCOHNYDTPRTFGGGLKEIKGGGSGG 114
Qy 121 GSGGGGSEVQLLEQSGAEIYRPGTSYKISCKASGAFYTNWLGWYKORPGHLEWIGDI 180
Db 115 GSGGGGSGVQ-LQPGAGRVYRPGASVYKLSCKASGYSTFTSMWNVKORPGGLEWIGMI 173
Qy 181 FPGSGNIHYNEKFKKATLTADKSSSTAYMQLSLTFEDSAVYPCARLRWDEPMYWGQ 240
Db 174 HPSDSETRLNQKFNDRATLTVDKYSTAYIQLSSPTSEDSAVYYCARGEYYGIFDYWGQ 233
Qy 241 GTTVYSSGGGSGDITKIQSGAEIARPGASVYKSGTSGYTFRTYTMWVYKORPGGLEW 300
Db 234 GTTVYSSGGGSGDITKIQSGAEIARPGASVYKSGTSGYTFRTYTMWVYKORPGGLEW 293
Qy 301 IGYINPBGYNTYNQKFKDRAKATLTDDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 360
Db 294 IGYINPBGYNTYNQKFKDRAKATLTDDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 353
Qy 361 YMGQGTTLTVSS 372
Db 354 YMRQGTTLTVSS 365

RESULT 3
US-10-672-932-18
; Sequence 18, Application US/10672932
; Publication No. US20050191702A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matchias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/10/672,932
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/948,004
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-672-932-18

Query Match 72.6%; Score 1484.5; DB 5; Length 495;
Best Local Similarity 74.7%; Pred. No. 4.2e-91;
Matches 278; Conservative 34; Mismatches 53; Indels 7; Gaps 2;

Qy 1 ELVMTGSSSLTVTAGEKVTMSCKSSQSLNSGNQKYLTVYQKPGQPPKLLIYMASTR 60
Db 1 DIVLTGSPASLASVGETVITTCRASENIY-----SYLAWYQKQKSPQLLYNAKTL 54
Qy 61 ESGVPRFTSGSGGTDTLTISSVQAEPLAVYVCOMDYSPYLTGAGTKLEIKGGGSGG 120
Db 55 TBGVPSRFGSGSGGTQSLKINSLOPEDFGNYFCOHNYDTPRTFGGGLKEIKGGGSGG 114
Qy 121 GSGGGGSEVQLLEQSGAEIYRPGTSYKISCKASGAFYTNWLGWYKORPGHLEWIGDI 180
Db 115 GSGGGGSGVQ-LQPGAGRVYRPGASVYKLSCKASGYSTFTSMWNVKORPGGLEWIGMI 173
Qy 181 FPGSGNIHYNEKFKKATLTADKSSSTAYMQLSLTFEDSAVYPCARLRWDEPMYWGQ 240
Db 174 HPSDSETRLNQKFNDRATLTVDKYSTAYIQLSSPTSEDSAVYYCARGEYYGIFDYWGQ 233
Qy 241 GTTVYSSGGGSGDITKIQSGAEIARPGASVYKSGTSGYTFRTYTMWVYKORPGGLEW 300
Db 234 GTTVYSSGGGSGDITKIQSGAEIARPGASVYKSGTSGYTFRTYTMWVYKORPGGLEW 293
Qy 301 IGYINPBGYNTYNQKFKDRAKATLTDDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 360
Db 294 IGYINPBGYNTYNQKFKDRAKATLTDDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 353
Qy 361 YMGQGTTLTVSS 372
Db 354 YMRQGTTLTVSS 365

RESULT 4
US-10-168-809-22
; Sequence 22, Application US/10168809
; Publication No. US20030180799A1
; GENERAL INFORMATION:
; APPLICANT: Muller-Hermelink, Hans Konrad
; APPLICANT: GREINER, AXEL
; APPLICANT: DORKEN, BERND
; APPLICANT: BARGOU, RALF
; APPLICANT: KUPER, PETER
; TITLE OF INVENTION: ANTIBODIES AGAINST PLASMA CELLS
; FILE REFERENCE: 009848-0272298
; CURRENT APPLICATION NUMBER: US/10/168,809
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/EP00/13238
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: DE 199 62 583.2
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic hybrid, no
; OTHER INFORMATION: natural origin
US-10-168-809-22

Query Match 71.7%; Score 1467; DB 4; Length 500;
Best Local Similarity 76.4%; Pred. No. 6.2e-90;
Matches 285; Conservative 29; Mismatches 55; Indels 4; Gaps 4;

QY 1 ELVWTPSSSLTVTAGKVTMSCKSSQSLNSGNQKNTLWYQKPGOPKLLIYMASTR 60
 Db 1 DIVWTPPLTLSTVIGQPASLSCKSSQSLNDS-DGKTYLNLQRPQSPRLISLVSKL 59
 QY 61 ESGVDRFTGSGSGTDFTLTISVQAEADLAVYVQNDYSYPLTFGAGTKLEIKGGGSGG 119
 Db 60 DSGVDRFTGSGSGTDFTLTISVQAEADLAVYVQNDYSYPLTFGAGTKLEIKGGGSGG 119
 QY 120 GGGSGGSGSEVQVLEQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 179
 Db 120 GGGSGGSGSEVQVLEQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 178
 QY 180 IFPGSGNHNKFKGKATLTADKSSSTAYVQSLTFEDSAVYPCARLRNMDPMDYWG 239
 Db 179 ISGVNPDRTYVQKFKGKATLTADKSSSTAYVQSLTFEDSAVYPCARLRNMDPMDYWG 237
 QY 240 QGTTVTVSSGGGSGSDIKLQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 299
 Db 238 QGTTVTVSSGGGSGSDIKLQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 297
 QY 300 WIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTFEDSAVYPCARYDDHYCL 359
 Db 298 WIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTFEDSAVYPCARYDDHYCL 357
 QY 360 DYMGGGTTLVSS 372
 Db 358 DYMGGGTTLVSS 370

RESULT 5

US-10-805-177-111
 ; Sequence 111, Application US/10805177
 ; Publication No. US20050084449a1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Bezabeh, Binyam
 ; APPLICANT: Foltz, Ian
 ; APPLICANT: Tse, Kam Fai
 ; APPLICANT: Jeffers, Michael
 ; APPLICANT: Meeri, Mehdi
 ; APPLICANT: Starling, Gary
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Khramtsov, Nikolai
 ; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
 ; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: ABCUR 006A
 ; CURRENT APPLICATION NUMBER: US/10/805,177
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: 60/456,652
 ; PRIOR FILING DATE: 2003-03-19
 ; NUMBER OF SEQ ID NOS: 141
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 111
 ; LENGTH: 499
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-10-805-177-111

Query Match 70.4%; Score 1439.5; DB 5; Length 499;
 Best Local Similarity 71.4%; Pred. No. 4,2e-88;
 Matches 270; Conservative 41; Mismatches 58; Indels 9; Gaps 3;

QY 1 ELVWTPSSSLTVTAGKVTMSCKSSQSLNSGNQKNTLWYQKPGOPKLLIYMASTR 60
 Db 1 DIVWTPPLTLSTVIGQPASLSCKSSQSLNDS-DGKTYLNLQRPQSPRLISLVSKL 59
 QY 61 ESGVDRFTGSGSGTDFTLTISVQAEADLAVYVQNDYSYPLTFGAGTKLEIKGGGSGG 120
 Db 61 ASGVDRFTGSGSGTDFTLTISVQAEADLAVYVQNDYSYPLTFGAGTKLEIKGGGSGG 120
 QY 121 GGGSGGSGSEVQVLEQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 180
 Db 121 GGGSGGSGSEVQVLEQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 180

Db 121 GGGSGGSGSEVQVLEQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 179
 QY 181 IFPGSGNHNKFKGKATLTADKSSSTAYVQSLTFEDSAVYPCARLRNMDPMDYWG 234
 Db 180 WYDSNKLVDYVGRFTIRDSNKNLTLQMSLRADPDAVYPCADYDNRSHHWG- 237
 QY 235 MDVWGGGTTTVSSGGGSGSDIKLQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 294
 Db 238 FDTWGGGTTTVSSGGGSGSDIKLQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 297
 QY 295 GQGLEWIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTFEDSAVYPCARYDDHYCL 354
 Db 298 GQGLEWIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTFEDSAVYPCARYDDHYCL 357
 QY 355 DHYCLDYMGGGTTLVSS 372
 Db 358 DHYCLDYMGGGTTLVSS 375

RESULT 6

US-10-682-845-59
 ; Sequence 59, Application US/10682845
 ; Publication No. US20040162411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lanzavecchia, Antonio
 ; TITLE OF INVENTION: Potent T cell modulating molecules
 ; FILE REFERENCE: G2296 US
 ; CURRENT APPLICATION NUMBER: US/10/682, 845
 ; CURRENT FILING DATE: 2003-10-10
 ; PRIOR APPLICATION NUMBER: US 60/419,149
 ; PRIOR FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: CA 2,403,313
 ; PRIOR FILING DATE: 2002-10-11
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 59
 ; LENGTH: 492
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; OTHER INFORMATION: scfv EpcAMxCD3 (modified antiCD3 VH-region derived from OKT-3)
 ; US-10-682-845-59

Query Match 69.1%; Score 1414; DB 4; Length 492;
 Best Local Similarity 71.2%; Pred. No. 2.1e-86;
 Matches 265; Conservative 43; Mismatches 54; Indels 10; Gaps 4;

QY 1 ELVWTPSSSLTVTAGKVTMSCKSSQSLNSGNQKNTLWYQKPGOPKLLIYMASTR 60
 Db 1 DIQLTOSQKFMSTSVGDVSVYTKRASQ-----NVTNVAVYQKPGSPKALISASVYR 54
 QY 61 ESGVDRFTGSGSGTDFTLTISVQAEADLAVYVQNDYSYPLTFGAGTKLEIKGGGSGG 120
 Db 55 YSGVDRFTGSGSGTDFTLTISVQAEADLAVYVQNDYSYPLTFGAGTKLEIKGGGSGG 114
 QY 121 GGGSGGSGSEVQVLEQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 180
 Db 115 GGGSGGSGSEVQVLEQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 173
 QY 181 IFPGSGNHNKFKGKATLTADKSSSTAYVQSLTFEDSAVYPCARLRNMDPMDYWG 240
 Db 174 WSG-GSTDYNAAFIRLSISKDNGSQVFFKMSIQANDTAIYCARHNNNS--FAYWQ 230
 QY 241 GTTVTVSSGGGSGSDIKLQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 300
 Db 231 GTTVTVSSGGGSGSDIKLQSGAEALVRPGTSVKISCKASGAFATNYMLGWKORPGHLEWIGD 290
 QY 301 IGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTFEDSAVYPCARYDDHYCL 360
 Db 291 IGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTFEDSAVYPCARYDDHYCL 350
 QY 361 YMGGGTTLTVSS 372
 Db 361 YMGGGTTLTVSS 372

```
Db      351 YMGQGTTLTVSS 362

RESULT 7
US-10-682-845-61
; Sequence 61, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: scfv EpcAMxCD3 with M1 mutant in anti-CD3 part
US-10-682-845-61

Query Match      68.9%; Score 1409; DB 4; Length 492;
Best Local Similarity 71.0%; Pred. No. 4.6e-86;
Matches 264; Conservative 44; Mismatches 54; Indels 10; Gaps 4;

Qy      1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNVLTWYQKPGQPPKLLIYMASTR 60
Db      1 DIQLTQSKRMSTSVGDRSVSTCKASQ-----NVGTNANVYQKPGQSKALITYSASTR 54
Qy      61 ESGVPRFTSGSGTDFTLTISVQAEADLAVVYCONDYSYPLTFGAGTKLEIKGGGSGG 120
Db      55 YSGVPRFTSGSGTDFTLTISVQAEADLAVVYCONDYSYPLTFGAGTKLEIKGGGSGG 114
Qy      121 GSGGGGSEVQLLEQSGAEIYRPGTSVKISCKASGAFNTYMWLGWYKORPGHLEMTGDI 180
Db      115 GSGGGGSGQYK-LQESGPGIYVPSQSLITCTVSGFSLTSGVHWVQSPKGLLEMTGVI 173
Qy      181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPEMDYMQ 240
Db      174 MSG-GSTDYNAATSRISLSDKNSKQVFFKMSLQANDTAITYCARMENMS--FAYMQ 230
Qy      241 GTTVTVSSGGGSDIKLQSGAEIARPGASVKNKSGTSGYTFRTYTMHWYKORPGGLEW 300
Db      231 GTTVTVSSGGGSDIKLQSGAEIARPGASVKNKSGTSGYTFRTYTMHWYKORPGGLEW 290
Qy      301 IGYNPSRGYTNVQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYVCARYYDDHYCLD 360
Db      291 IGYNPSRGYTNVQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYVCARYYDDHYCLD 350
Qy      361 YMGQGTTLTVSS 372
Db      351 YMGQGTTLTVSS 362

RESULT 8
US-10-682-845-87
; Sequence 87, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
```

```
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: scfv EpcAMxCD3 with M76 mutant in anti-CD3 part
US-10-682-845-87

Query Match      68.8%; Score 1407; DB 4; Length 492;
Best Local Similarity 71.0%; Pred. No. 6.2e-86;
Matches 264; Conservative 44; Mismatches 54; Indels 10; Gaps 4;

Qy      1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNVLTWYQKPGQPPKLLIYMASTR 60
Db      1 DIQLTQSKRMSTSVGDRSVSTCKASQ-----NVGTNANVYQKPGQSKALITYSASTR 54
Qy      61 ESGVPRFTSGSGTDFTLTISVQAEADLAVVYCONDYSYPLTFGAGTKLEIKGGGSGG 120
Db      55 YSGVPRFTSGSGTDFTLTISVQAEADLAVVYCONDYSYPLTFGAGTKLEIKGGGSGG 114
Qy      121 GSGGGGSEVQLLEQSGAEIYRPGTSVKISCKASGAFNTYMWLGWYKORPGHLEMTGDI 180
Db      115 GSGGGGSGQYK-LQESGPGIYVPSQSLITCTVSGFSLTSGVHWVQSPKGLLEMTGVI 173
Qy      181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPEMDYMQ 240
Db      174 MSG-GSTDYNAATSRISLSDKNSKQVFFKMSLQANDTAITYCARMENMS--FAYMQ 230
Qy      241 GTTVTVSSGGGSDIKLQSGAEIARPGASVKNKSGTSGYTFRTYTMHWYKORPGGLEW 300
Db      231 GTTVTVSSGGGSDIKLQSGAEIARPGASVKNKSGTSGYTFRTYTMHWYKORPGGLEW 290
Qy      301 IGYNPSRGYTNVQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYVCARYYDDHYCLD 360
Db      291 IGYNPSRGYTNVQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYVCARYYDDHYCLD 350
Qy      361 YMGQGTTLTVSS 372
Db      351 YMGQGTTLTVSS 362

RESULT 9
US-10-682-845-65
; Sequence 65, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: scfv EpcAMxCD3 with M7 mutant in anti-CD3 part
US-10-682-845-65

Query Match      68.7%; Score 1406; DB 4; Length 492;
Best Local Similarity 71.0%; Pred. No. 7.2e-86;
Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;

Qy      1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNVLTWYQKPGQPPKLLIYMASTR 60
```

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Db      1 DIQLTOSQKFMSTSVGDRVSVTCASQ-----NVGTVNAVYQKPGQSPKALIYSASR 54
QY      61 ESGVDPDFTSGSGSDTFTLTISVQAEPLAVYCCNDPSYPLTFGAGTKLEIKGGGSGG 120
Db      55 YSGVDPDFTSGSGSDTFTLTISNVQSEDLAEYFCQOQNSYPLTFGAGTKLEIKGGGSGG 114
QY      121 GSGGGGSEVQLLEBSGAELVRPGTSVKISCKASGYAFNNYMLGWYKORPGHLEWIGDI 180
Db      115 GSGGGGSGQVK-LQESGPGELVQPSQSLITCTVSGFSLTSYGVMWRQSPKGLEMLGVI 173
QY      181 PRSGGNHYNKFKGKATLTLDKSSSTAYMQLSLTFEDSAVYFCARLNMDEPMDYWGQ 240
Db      174 WSG-GSTDYNAFISRLSISDKNSQYVFFKNLSIQANDTAIYCARMENMS--PAYWGQ 230
QY      241 GTTVTVSSGGGSDIKLQSGAELARPGASVMSCKTSYFTFRYTMHVMKORPGGLEW 300
Db      231 GTTVTVSSGGGSDIKLQSGAELARPGASVMSCKTSYFTFRYTMHVMKORPGGLEW 290
QY      301 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCLD 360
Db      291 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCLD 350
QY      361 YMGQGTTLTVSS 372
Db      351 YMGQGTTLTVSS 362

```

RESULT 10
US-10-682-845-67
; Sequence 67, Application US/10682845
; Publication No. US20040162411A1

```

GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating molecules
FILE REFERENCE: G2296 US
CURRENT FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 492
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: scFv EpcAMxCD3 with M9 mutant in anti-CD3 part
US-10-682-845-67

```

Query Match 68.7%; Score 1406; DB 4; Length 492;
Best Local Similarity 71.0%; Pred. No. 7.2e-86;
Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;

```

QY      1 ELVMTQSPSSLTAVTAGEKYTWSCSKSQSLNSGNQKNTLVYQKRGQPPKLLIYASTR 60
Db      1 DIQLTOSQKFMSTSVGDRVSVTCASQ-----NVGTVNAVYQKPGQSPKALIYSASR 54
QY      61 ESGVDPDFTSGSGSDTFTLTISVQAEPLAVYCCNDPSYPLTFGAGTKLEIKGGGSGG 120
Db      55 YSGVDPDFTSGSGSDTFTLTISNVQSEDLAEYFCQOQNSYPLTFGAGTKLEIKGGGSGG 114
QY      121 GSGGGGSEVQLLEBSGAELVRPGTSVKISCKASGYAFNNYMLGWYKORPGHLEWIGDI 180
Db      115 GSGGGGSGQVK-LQESGPGELVQPSQSLITCTVSGFSLTSYGVMWRQSPKGLEMLGVI 173
QY      181 PRSGGNHYNKFKGKATLTLDKSSSTAYMQLSLTFEDSAVYFCARLNMDEPMDYWGQ 240
Db      174 WSG-GSTDYNAFISRLSISDKNSQYVFFKNLSIQANDTAIYCARMENMS--PAYWGQ 230
QY      241 GTTVTVSSGGGSDIKLQSGAELARPGASVMSCKTSYFTFRYTMHVMKORPGGLEW 300

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Db      231 GTTVTVSSGGGSDIKLQSGAELARPGASVMSCKTSYFTFRYTMHVMKORPGGLEW 290
QY      301 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCLD 360
Db      291 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCLD 350
QY      361 YMGQGTTLTVSS 372
Db      351 YMGQGTTLTVSS 362

```

RESULT 11
US-10-682-845-63
; Sequence 63, Application US/10682845
; Publication No. US20040162411A1

```

GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating molecules
FILE REFERENCE: G2296 US
CURRENT FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 492
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: scFv EpcAMxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-63

```

Query Match 68.7%; Score 1405; DB 4; Length 492;
Best Local Similarity 71.0%; Pred. No. 8.4e-86;
Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;

```

QY      1 ELVMTQSPSSLTAVTAGEKYTWSCSKSQSLNSGNQKNTLVYQKRGQPPKLLIYASTR 60
Db      1 DIQLTOSQKFMSTSVGDRVSVTCASQ-----NVGTVNAVYQKPGQSPKALIYSASR 54
QY      61 ESGVDPDFTSGSGSDTFTLTISVQAEPLAVYCCNDPSYPLTFGAGTKLEIKGGGSGG 120
Db      55 YSGVDPDFTSGSGSDTFTLTISNVQSEDLAEYFCQOQNSYPLTFGAGTKLEIKGGGSGG 114
QY      121 GSGGGGSEVQLLEBSGAELVRPGTSVKISCKASGYAFNNYMLGWYKORPGHLEWIGDI 180
Db      115 GSGGGGSGQVK-LQESGPGELVQPSQSLITCTVSGFSLTSYGVMWRQSPKGLEMLGVI 173
QY      181 PRSGGNHYNKFKGKATLTLDKSSSTAYMQLSLTFEDSAVYFCARLNMDEPMDYWGQ 240
Db      174 WSG-GSTDYNAFISRLSISDKNSQYVFFKNLSIQANDTAIYCARMENMS--PAYWGQ 230
QY      241 GTTVTVSSGGGSDIKLQSGAELARPGASVMSCKTSYFTFRYTMHVMKORPGGLEW 300
Db      231 GTTVTVSSGGGSDIKLQSGAELARPGASVMSCKTSYFTFRYTMHVMKORPGGLEW 290
QY      301 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCLD 360
Db      291 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCLD 350
QY      361 YMGQGTTLTVSS 372
Db      351 YMGQGTTLTVSS 362

```

RESULT 12
US-10-682-845-71
; Sequence 71, Application US/10682845
; Publication No. US20040162411A1

```

; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: scfv EPCAMxCD3 with M1 mutant in anti-CD3 part
US-10-682-845-71

```

```

Query Match      68.7%; Score 1405; DB 4; Length 492;
Best Local Similarity 70.7%; Pred. No. 8.4e-86;
Matches 263; Conservative 45; Mismatches 54; Indels 10; Gaps 4;

```

```

QY 1 ELVMTGSPSSLVTYTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DIQLTQSKFMSTSVGDRLSVYTCASQ-----NVGTNAVYQKPGQSPKALIIYSASR 54

QY 61 ESGVPRFTGSGGSDTFTLTITSSVQAEADLAVYQNDYSPYLTFGAGTKLEIKGGGSGG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 55 YSGVPRFTGSGGSDTFTLTITSSVQAEADLAVYQNDYSPYLTFGAGTKLEIKGGGSGG 114

QY 121 GSGGGGSEVQLLEQSGAEIYRPGTSYKISCKASGVAFTNWMVKORPGHLEWIGDI 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 115 GSGGGGSGQVK-LQESGPGIYVQPSQSLITCTVSGPSTISYGVWVQSPKGLIEMIGVI 173

QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 WSG-GSTDYNAAFISRLSISKDNSKQVFFKMSLQANDTAIYCAEMENWS--FAVWQ 230

QY 241 GTTIVTSSGGGSDIKLQSGAEIARPGASVKNKCTSGYTFRTYTMHWVKORPGGLEW 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 231 GTTIVTSSGGGSDIKLQSGAEIARPGASVKNKCTSGYTFRTYTMHWVKORPGGLEW 290

QY 301 IGYINPGRGTNNYQKFKDKATLTDDKSSSTAYWQLSLTSEDSAVYVCARYDDHYCLD 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 291 IGYINPGRGTNNYQKFKDKATLTDDKSSSTAYWQLSLTSEDSAVYVCARYDDHYCLD 350

QY 361 YMGQGTTLTVSS 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 351 YMGQGTTLTVSS 362

```

```

RESULT 13
US-10-682-845-69
; Sequence 69, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence

```

```

; FEATURE:
; OTHER INFORMATION: scfv EPCAMxCD3 with M10 mutant in anti-CD3 part
US-10-682-845-69

```

```

Query Match      68.6%; Score 1404; DB 4; Length 492;
Best Local Similarity 71.0%; Pred. No. 9.8e-86;
Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;

```

```

QY 1 ELVMTGSPSSLVTYTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DIQLTQSKFMSTSVGDRLSVYTCASQ-----NVGTNAVYQKPGQSPKALIIYSASR 54

QY 61 ESGVPRFTGSGGSDTFTLTITSSVQAEADLAVYQNDYSPYLTFGAGTKLEIKGGGSGG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 55 YSGVPRFTGSGGSDTFTLTITSSVQAEADLAVYQNDYSPYLTFGAGTKLEIKGGGSGG 114

QY 121 GSGGGGSEVQLLEQSGAEIYRPGTSYKISCKASGVAFTNWMVKORPGHLEWIGDI 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 115 GSGGGGSGQVK-LQESGPGIYVQPSQSLITCTVSGPSTISYGVWVQSPKGLIEMIGVI 173

QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 WSG-GSTDYNAAFISRLSISKDNSKQVFFKMSLQANDTAIYCAEMENWS--FAVWQ 230

QY 241 GTTIVTSSGGGSDIKLQSGAEIARPGASVKNKCTSGYTFRTYTMHWVKORPGGLEW 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 231 GTTIVTSSGGGSDIKLQSGAEIARPGASVKNKCTSGYTFRTYTMHWVKORPGGLEW 290

QY 301 IGYINPGRGTNNYQKFKDKATLTDDKSSSTAYWQLSLTSEDSAVYVCARYDDHYCLD 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 291 IGYINPGRGTNNYQKFKDKATLTDDKSSSTAYWQLSLTSEDSAVYVCARYDDHYCLD 350

QY 361 YMGQGTTLTVSS 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 351 YMGQGTTLTVSS 362

```

```

RESULT 14
US-10-682-845-73
; Sequence 73, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: scfv EPCAMxCD3 with M13 mutant in anti-CD3 part
US-10-682-845-73

```

```

Query Match      68.5%; Score 1401; DB 4; Length 492;
Best Local Similarity 70.7%; Pred. No. 1.6e-85;
Matches 263; Conservative 44; Mismatches 55; Indels 10; Gaps 4;

```

```

QY 1 ELVMTGSPSSLVTYTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DIQLTQSKFMSTSVGDRLSVYTCASQ-----NVGTNAVYQKPGQSPKALIIYSASR 54

QY 61 ESGVPRFTGSGGSDTFTLTITSSVQAEADLAVYQNDYSPYLTFGAGTKLEIKGGGSGG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 55 YSGVPRFTGSGGSDTFTLTITSSVQAEADLAVYQNDYSPYLTFGAGTKLEIKGGGSGG 114

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:12 ; Search time 89 Seconds
(without alignments)
1866.126 Million cell updates/sec

Title: US-10-743-697-1
Perfect score: 2046
Sequence: 1 ELVMTQSPSSITVTAGEKVT.....LDYWGCGTTLTVSSHHHHH 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_21:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*
 - 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2046	100.0	378	9	AEA36900 Anti-CD3x
2	1998	97.7	521	9	ADV66121 Anti-CD3-
3	1935	94.6	521	9	ADV66116 Anti-CD3-
4	1930	94.3	496	9	ADZ83653 CD3 speci
5	1930	94.3	496	9	ADZ83637 CD3 speci
6	1930	94.3	496	9	ADZ83645 CD3 speci
7	1892	92.5	496	9	ADZ83615 CD3 speci
8	1892	92.5	496	9	ADZ83629 CD3 speci
9	1882	92.5	515	9	ADZ83441 Deimmuniz
10	1859	90.9	496	9	ADZ83641 CD3 speci
11	1859	90.9	496	9	ADZ83649 CD3 speci
12	1859	90.9	496	9	ADZ83657 CD3 speci
13	1829	89.4	515	9	ADZ83436 Deimmuniz
14	1821	89.0	496	9	ADZ83619 CD3 speci
15	1821	89.0	496	9	ADZ83625 CD3 speci
16	1821	89.0	496	9	ADZ83633 CD3 speci
17	1821	89.0	496	9	ADZ83633 CD3 speci
18	1677	84.6	515	9	ADV66113 Anti-CD3-
19	1625	79.4	506	9	ADZ83427 Mature fo
20	1623	78.9	494	9	ADZ83427 Deimmuniz
21	1614.5	78.9	526	9	ADV66107 Anti-CD3-
22	1613.5	78.9	501	9	ADV61529 Mature fo
23	1611.5	78.8	495	9	ADV61527 Mature fo
24	1609.5	78.7	526	9	ADV66119 Anti-CD3-

25	1581	77.3	498	9	ADZ83582 Non-deimm
26	1581	77.3	504	9	ADV14556 Bioprectifi
27	1581	77.3	504	9	AEA52447 Human CD3
28	1581	77.3	531	3	AAV43749 Amino aci
29	1562	76.3	504	9	ADV21535 Mature fo
30	1548.5	75.7	502	9	ADV14530 Bioprectifi
31	1513	73.9	498	9	ADZ83574 Vector PE
32	1513	73.9	498	9	ADZ83578 Vector PE
33	1513	73.9	498	9	ADZ83576 Vector PE
34	1508.5	73.7	520	9	ADZ83433 Deimmuniz
35	1503.5	73.5	520	9	ADZ83439 Deimmuniz
36	1484.5	72.6	495	5	AAE22193 Murine CC
37	1475	72.1	498	9	ADZ83572 Vector PE
38	1475	72.1	498	9	ADZ83568 Vector PE
39	1475	72.1	498	9	ADZ83570 Vector PE
40	1470	71.8	498	9	ADZ83558 Vector PE
41	1470	71.8	498	9	ADZ83556 Vector PE
42	1470	71.8	498	9	ADZ83560 Vector PE
43	1466	71.7	498	9	ADZ83564 Vector PE
44	1466	71.7	498	9	ADZ83566 Vector PE
45	1466	71.7	498	9	ADZ83562 Vector PE

ALIGNMENTS

RESULT 1
AEA36900
ID AEA36900 standard; protein; 378 AA.
XX
AC AEA36900;
DT 25-AUG-2005 (first entry)
XX
DE Anti-CD3xanti-EpCAM bispecific chimeric antibody.
KM chimeric antibody; cytostatic; antimicrobial; antiallergic;
KM antinflammatory; virucide; antiparasitic; immunomodulatory;
KM immunosuppressive; vaccine; bispecific antibody; cancer; inflammation;
KM immune disorder; infection; viral infection; allergy;
KM parasitic infection; graft versus host disease.
OS Synthetic.
XX
PN US2005136050-A1.
XX
PD 23-JUN-2005.
XX
PF 22-DEC-2003; 2003US-00743697.
XX
PR 22-DEC-2003; 2003US-00743697.
XX
PA (KUPF/) KUPFER P.
PA (BAER/) BAUERLE P.
PA (ITIN/) ITIN C.
PI Kufer P, Berry M, Baeuerle P, Itin C;
XX
DR WPI; 2005-444079/45.
XX
PT New bispecific antibody comprising two antibody variable domains on a
PT single polypeptide chain, useful in preparing a composition for treating
PT or preventing proliferative, infectious or graft-versus-
PT host disease.
XX
PS Claim 24; SEQ ID NO 1; 12pp; English.
XX
CC The invention relates to a bispecific antibody comprising two antibody
CC variable domains on a single polypeptide chain, where a first portion of
CC the bispecific antibody is capable of recruiting the activity of a human
CC immune effector cell by specifically binding to an effector antigen
CC located on the human immune effector cell, the first portion consisting

CC of one antibody variable domain; and a second portion of the bispecific
 CC antibody is capable of specifically binding to a target antigen other
 CC than the effector antigen, the target antigen being located on a target
 CC cell other than the human immune effector cell, and the second portion
 CC comprising an antibody variable domain. The bispecific antibody is useful
 CC in preparing a composition for treating, preventing or ameliorating a
 CC proliferative disease, a tumorous disease, an inflammatory disease, an
 CC immunological disorder, an autoimmune disease, an infectious disease, a
 CC viral disease, an allergic reaction, a parasitic reaction, a graft-versus
 CC -host disease or a host-versus-graft disease. This sequence corresponds
 CC to the chimeric anti-CD3xanti-EpCAM bispecific antibody of the invention.

XX Sequence 378 AA;

Query Match 100.0%; Score 2046; DB 9; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.1e-119;
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKLLIYMSTR 60
 DB 1 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKLLIYMSTR 60
 QY 61 ESGVPRFRTSGSGDTFTLTSSVQAEADLAVYCONDYSPFLFGAGTKLEIKGGGSGG 120
 DB 61 ESGVPRFRTSGSGDTFTLTSSVQAEADLAVYCONDYSPFLFGAGTKLEIKGGGSGG 120
 QY 121 GSGGGGSEVQLLQSGAEIYRPQTSYKISCKASGYFTNMYLGMVKORPGHGLEWIGDI 180
 DB 121 GSGGGGSEVQLLQSGAEIYRPQTSYKISCKASGYFTNMYLGMVKORPGHGLEWIGDI 180
 QY 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRWDEPMDYWGQ 240
 DB 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRWDEPMDYWGQ 240
 QY 241 GTTAVTSSGGGSDIKLQSGAEIARPGASVMSCKTSGYTFRTYTHMWVKORPGGLEW 300
 DB 241 GTTAVTSSGGGSDIKLQSGAEIARPGASVMSCKTSGYTFRTYTHMWVKORPGGLEW 300
 QY 301 IGYINPGRGYTNYNQKFKDRAITLTDKSSSTAYWQLSLTFEDSAVYFCARYYDDHYCLD 360
 DB 301 IGYINPGRGYTNYNQKFKDRAITLTDKSSSTAYWQLSLTFEDSAVYFCARYYDDHYCLD 360
 QY 361 YMGQGTTLTVSSSHHHHHH 378
 DB 361 YMGQGTTLTVSSSHHHHHH 378

RESULT 2
 ADV66121 ID ADV66121 standard; protein; 521 AA.

XX AC ADV66121;

XX DT 24-FEB-2005 (first entry)

XX DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 44.

XX KW bispecific single chain antibody; epithelial cell adhesion molecule;
 KW EpCAM; CD3; tumor; cancer; cytostatic.

XX OS Unidentified.

XX PN WO2004106383-A1.

XX PD 09-DEC-2004.

XX PF 26-MAY-2004; 2004WO-BP005687.

XX PR 31-MAY-2003; 2003EP-00012133.

XX PR 31-MAY-2003; 2003EP-00012134.

XX PA (MICR-) MICROMET AG.

PI Kufner P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkner-Schuetz U, Baeuerle P;

XX WPI; 2005-021271/02.

DR N-PSDB; ADV66120.

XX PT New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.

PS Claim 12; SEQ ID NO 44; 227bp; English.

XX The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.

XX Sequence 521 AA;

Query Match 97.7%; Score 1998; DB 9; Length 521;
 Best Local Similarity 100.0%; Pred. No. 1.5e-116;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKLLIYMSTR 60
 DB 20 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKLLIYMSTR 79
 QY 61 ESGVPRFRTSGSGDTFTLTSSVQAEADLAVYCONDYSPFLFGAGTKLEIKGGGSGG 120
 DB 80 ESGVPRFRTSGSGDTFTLTSSVQAEADLAVYCONDYSPFLFGAGTKLEIKGGGSGG 139
 QY 121 GSGGGGSEVQLLQSGAEIYRPQTSYKISCKASGYFTNMYLGMVKORPGHGLEWIGDI 180
 DB 140 GSGGGGSEVQLLQSGAEIYRPQTSYKISCKASGYFTNMYLGMVKORPGHGLEWIGDI 199
 QY 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRWDEPMDYWGQ 240
 DB 200 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRWDEPMDYWGQ 259
 QY 241 GTTAVTSSGGGSDIKLQSGAEIARPGASVMSCKTSGYTFRTYTHMWVKORPGGLEW 300
 DB 260 GTTAVTSSGGGSDIKLQSGAEIARPGASVMSCKTSGYTFRTYTHMWVKORPGGLEW 319
 QY 301 IGYINPGRGYTNYNQKFKDRAITLTDKSSSTAYWQLSLTFEDSAVYFCARYYDDHYCLD 360
 DB 320 IGYINPGRGYTNYNQKFKDRAITLTDKSSSTAYWQLSLTFEDSAVYFCARYYDDHYCLD 379
 QY 361 YMGQGTTLTVSS 372
 DB 380 YMGQGTTLTVSS 391

RESULT 3
 ADV66116 ID ADV66116 standard; protein; 521 AA.

XX AC ADV66116;

XX DT 24-FEB-2005 (first entry)

XX DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 39.

XX KW bispecific single chain antibody; epithelial cell adhesion molecule;
 KW EpCAM; CD3; tumor; cancer; cytostatic.

XX OS Unidentified.

XX PN WO2004106383-A1.

PD 09-DEC-2004.
 XX
 XX 26-MAY-2004; 2004MO-EP005687.
 PF
 XX
 PR 31-MAY-2003; 2003EP-00012133.
 PR 31-MAY-2003; 2003EP-00012134.
 XX
 XX (MICR-) MICROMET AG.
 XX
 XX Kiefer P, Berry M, Offner S, Brieschwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkeri-Schuetz U, Baeuerle P;
 DR WPI; 2005-021271/02.
 DR N-PSDB; ADV66115.
 XX
 XX New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.
 PS Claim 12; SEQ ID NO 39; 227pp; English.
 XX
 XX The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.
 CC
 XX Sequence 521 AA;
 SQ
 Query Match 94.6%; Score 1935; DB 9; Length 521;
 Best Local Similarity 97.0%; Pred. No. 1.2e-112;
 Matches 361; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ELVMTQSPSSSLVTAVTAGEKVTWMSCKSSQSLNSGNKNTLTWYQKRGQPPKLLIYMASTR 60
 DB 20 ELVMTQSPSSSLVSAAGEKVTWMSCKSSQSLNSGNKNTLTWYQKRGQPPKLLIYGASTR 79
 QY 61 ESGVDRFTGSGSGTDFTLTITSSVQAEDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 120
 DB 80 ESGVDRFTGSGSGTDFTLTITSSVQAEDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 139
 QY 121 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFTNMYLGWVKORPGHGLEWIGDI 180
 DB 140 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFTNMYLGWVKORPGHGLEWIGDI 199
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPEMDYMQ 240
 DB 200 FPGSGNAHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPEMDYMQ 259
 QY 241 GTTIVTSSGGGSDIKLQOQSGAEIVRPGASVYMSCKTSYTRTTRTMHVVKORPGQGLEW 300
 DB 260 GTTIVTSSGGGSDIKLQOQSGAEIVRPGASVYMSCKTSYTRTTRTMHVVKORPGQGLEW 319
 QY 301 IGYINPSRGYTNVKKFKQKATLTLDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCID 360
 DB 320 IGYINPSRGYTNVKKFKQKATLTLDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCID 379
 QY 361 YWGQGTLLTVSS 372
 DB 380 YWGQGTLLTVSS 391
 RESULT 4
 ADZ83653
 ID ADZ83653 standard; protein; 496 AA.
 XX
 AC ADZ83653;
 XX
 DT 14-JUL-2005 (first entry)
 XX

DE CD3 specific binding construct SEQ ID NO 275.
 XX
 XX neoplasm; inflammation; immune disorder; infection; allergy;
 KM graft versus host disease; cytostatic; antineoplastic;
 KM immunosuppressive; virucide; antibacterial; anti-allergic; antiparasitic.
 XX
 XX Synthetic.
 OS
 XX WO2005040220-A1.
 XX
 XX 06-MAY-2005.
 XX
 XX 15-OCT-2004; 2004MO-EP011646.
 XX
 XX 16-OCT-2003; 2003EP-00023581.
 XX
 XX (MICR-) MICROMET AG.
 XX
 XX Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;
 PI Carr FU, Hamilton AA, Williams S;
 DR WPI; 2005-333494/34.
 DR N-PSDB; ADZ83652.
 XX
 XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a CD3 specific binding construct.
 CC
 XX Sequence 496 AA;
 SQ
 Query Match 94.3%; Score 1930; DB 9; Length 496;
 Best Local Similarity 95.2%; Pred. No. 2.4e-112;
 Matches 354; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ELVMTQSPSSSLVTAVTAGEKVTWMSCKSSQSLNSGNKNTLTWYQKRGQPPKLLIYMASTR 60
 DB 1 ELVMTQSPSSSLVTAVTAGEKVTWMSCKSSQSLNSGNKNTLTWYQKRGQPPKLLIYMASTR 60
 QY 61 ESGVDRFTGSGSGTDFTLTITSSVQAEDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 120
 DB 61 ESGVDRFTGSGSGTDFTLTITSSVQAEDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 120
 QY 121 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFTNMYLGWVKORPGHGLEWIGDI 180
 DB 121 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFTNMYLGWVKORPGHGLEWIGDI 180
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPEMDYMQ 240
 DB 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPEMDYMQ 240
 QY 241 GTTIVTSSGGGSDIKLQOQSGAEIVRPGASVYMSCKTSYTRTTRTMHVVKORPGQGLEW 300
 DB 241 GTTIVTSSGGGSDIKLQOQSGAEIVRPGASVYMSCKTSYTRTTRTMHVVROAPGQGLEW 300

QY 301 IGYINPSRGYTNYNQKFKDRAITLTTDKSSSTAYWQLSLTSBDSAVYVCARYYDDHYCLD 360
 DB 301 IGYINPSRGYTNYNQKFKDRVITITTDKSTSTAYWELSSLSEDEPTAVYVCARYYDDHYCLD 360
 QY 361 YMGQGITLTVSS 372
 DB 361 YMGQGITVTVSS 372

RESULT 5

AD283637
 ID AD283637 standard; protein; 496 AA.

AC AD283637;

DT 14-JUL-2005 (first entry)

DE CD3 specific binding construct SEQ ID NO 259.

XX neoplasm; inflammation; immune disorder; infection; allergy;

KM graft versus host disease; Cytostatic; Antiinflammatory;

KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.

OS Synthetic.

PN W02005040220-A1.

PD 06-MAY-2005.

PP 15-OCT-2004; 2004WO-EP011646.

PR 16-OCT-2003; 2003EP-00023581.

XX (MICR-) MICROMET AG.

PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,

PI Carr FJ, Hamilton AA, Williams S;

XX WPI; 2005-333494/34.

DR N-PSDB; AD283636.

XX

PS Claim 20; SEQ ID NO 259; 639pp; English.

XX

CC The invention relates to a cytotoxically active CD3 specific binding

CC construct comprising a first domain specifically binding to human CD3 and

CC an Ig-derived second binding domain. The CD3 specific binding construct

CC above or the construct produced by the process, nucleic acid molecule,

CC vector, or host is useful for the preparation of a pharmaceutical

CC composition for the prevention, treatment, or amelioration of a

CC proliferative disease, a tumor, an inflammatory disease, an immunological

CC disorder, an autoimmune disease, an infectious disease, viral disease,

CC allergic reactions, parasitic reactions, graft-versus-host diseases, or

CC host-versus-graft diseases. The present sequence represents the amino

CC acid sequence of a CD3 specific binding construct.

XX

SQ Sequence 496 AA;

Query Match 94.3%; Score 1930; DB 9; Length 496;

Best Local Similarity 95.2%; Pred. No. 2.4e-112; Indels 0; Gaps 0;

Matches 354; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSLTITVAAGEKVTWMSCKSSQSLNSGNQKNTLWYQKPGQPKRLIYMASTR 60

DB 1 ELVMTQSPSSLTITVAAGEKVTWMSCKSSQSLNSGNQKNTLWYQKPGQPKRLIYMASTR 60
 QY 61 ESGVDPFRFGSGSGGTFTLTISVQAEADLAVYVCQNDYGYPLTFGAGTKLEIKGSGSGG 120
 DB 61 ESGVDPFRFGSGSGGTFTLTISVQAEADLAVYVCQNDYGYPLTFGAGTKLEIKGSGSGG 120
 QY 121 GSGGSGSGSEVQLEQSGAEIVRPGTSVKISCKASGYAFTNMYLGMVKQRPQGLIEWIGDI 180
 DB 121 GSGGSGSGSEVQLEQSGAEIVRPGTSVKISCKASGYAFTNMYLGMVKQRPQGLIEWIGDI 180
 QY 181 PRSGNIIHYNEKKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRWDEPMYWGQ 240
 DB 181 PRSGNIIHYNEKKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRWDEPMYWGQ 240
 QY 241 GTTVTVSSGGGSDIKLQSGAEIARPGASVKNKSCGTSGYFTFRYTMHWYKQRPQGLIEW 300
 DB 241 GTTVTVSSGGGSDIKLQSGAEIARPGASVKNKSCGTSGYFTFRYTMHWYKQRPQGLIEW 300
 QY 301 IGYINPSRGYTNYNQKFKDRAITLTTDKSSSTAYWQLSLTSBDSAVYVCARYYDDHYCLD 360
 DB 301 IGYINPSRGYTNYNQKFKDRVITITTDKSTSTAYWELSSLSEDEPTAVYVCARYYDDHYCLD 360
 QY 361 YMGQGITLTVSS 372
 DB 361 YMGQGITVTVSS 372

RESULT 6

AD283645
 ID AD283645 standard; protein; 496 AA.

AC AD283645;

DT 14-JUL-2005 (first entry)

DE CD3 specific binding construct SEQ ID NO 267.

XX neoplasm; inflammation; immune disorder; infection; allergy;

KM graft versus host disease; Cytostatic; Antiinflammatory;

KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.

OS Synthetic.

PN W02005040220-A1.

PD 06-MAY-2005.

PP 15-OCT-2004; 2004WO-EP011646.

PR 16-OCT-2003; 2003EP-00023581.

XX (MICR-) MICROMET AG.

PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,

PI Carr FJ, Hamilton AA, Williams S;

XX WPI; 2005-333494/34.

DR N-PSDB; AD283644.

XX

PS Claim 20; SEQ ID NO 267; 639pp; English.

XX

CC The invention relates to a cytotoxically active CD3 specific binding

CC construct comprising a first domain specifically binding to human CD3 and

CC an Ig-derived second binding domain. The CD3 specific binding construct

CC above or the construct produced by the process, nucleic acid molecule,

CC vector, or host is useful for the preparation of a pharmaceutical

CC composition for the prevention, treatment, or amelioration of a

CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxicity active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a CD3 specific binding construct.

XX Sequence 496 AA;

Query Match 94.3%; Score 1930; DB 9; Length 496;
 Best Local Similarity 95.2%; Pred. No. 2.4e-112;
 Matches 354; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSSLTVNAGEKVTWMSCKSSQSLNSGNQKYLTVYQKPGQPKLLIYMASTR 60
 DB 1 ELVMTQSPSSSLTVNAGEKVTWMSCKSSQSLNSGNQKYLTVYQKPGQPKLLIYMASTR 60
 QY 61 ESGVPDRFTGSGSGDTFTLTISVQAEIDLAVYYCONDYSPYLTFGAGTKLEIKGGGSGG 120
 DB 61 ESGVPDRFTGSGSGDTFTLTISVQAEIDLAVYYCONDYSPYLTFGAGTKLEIKGGGSGG 120
 QY 121 GSGSGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFNYWLGWVKORPGHGLEWIGDI 180
 DB 121 GSGSGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFNYWLGWVKORPGHGLEWIGDI 180
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
 DB 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
 QY 241 GTTAVTSSGGGSDIKLQSGAEIVRPGTSVKISCKASGYAFNYWLGWVKORPGHGLEW 300
 DB 241 GTTAVTSSGGGSDIKLQSGAEIVRPGTSVKISCKASGYAFNYWLGWVKORPGHGLEW 300
 QY 301 IGYINPSRGYNNYQKFDKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 360
 DB 301 IGYINPSRGYNNYQKFDKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 360
 QY 361 YWGQGTTLTVSS 372
 DB 361 YWGQGTTLTVSS 372

RESULT 7
 AD283615
 ID AD283615 standard; protein; 496 AA.

XX AC AD283615;
 XX DT 14-JUL-2005 (first entry)
 XX DE CD3 specific binding construct SEQ ID NO 237.
 XX KM neoplasm; inflammation; immune disorder; infection; allergy;
 XX KM graft versus host disease; cytotoxicity; antiinflammatory;
 XX KM immunosuppressive; vitruide; antibacterial; antiallergic; antiparasitic.
 XX OS Synthetic.
 XX PN MO2005040220-AL.
 XX PD 06-MAY-2005.
 XX PF 15-OCT-2004; 2004MO-EP011646.
 XX PR 16-OCT-2003; 2003EP-00023581.
 XX PA (MICR-) MICROMET AG.
 XX PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baueerle P;

PI Carr FJ, Hamilton AA, Williams S;
 XX WPI; 2005-333494/34.
 DR N-PSDB; AD283614.
 XX New cytotoxicity active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.
 XX Claim 20; SEQ ID NO 237; 639pp; English.

XX The invention relates to a cytotoxicity active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxicity active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a CD3 specific binding construct.

XX Sequence 496 AA;

Query Match 92.5%; Score 1892; DB 9; Length 496;
 Best Local Similarity 93.5%; Pred. No. 5.6e-110;
 Matches 348; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSSLTVNAGEKVTWMSCKSSQSLNSGNQKYLTVYQKPGQPKLLIYMASTR 60
 DB 1 ELVMTQSPSSSLTVNAGEKVTWMSCKSSQSLNSGNQKYLTVYQKPGQPKLLIYMASTR 60
 QY 61 ESGVPDRFTGSGSGDTFTLTISVQAEIDLAVYYCONDYSPYLTFGAGTKLEIKGGGSGG 120
 DB 61 ESGVPDRFTGSGSGDTFTLTISVQAEIDLAVYYCONDYSPYLTFGAGTKLEIKGGGSGG 120
 QY 121 GSGSGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFNYWLGWVKORPGHGLEWIGDI 180
 DB 121 GSGSGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFNYWLGWVKORPGHGLEWIGDI 180
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
 DB 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
 QY 241 GTTAVTSSGGGSDIKLQSGAEIVRPGTSVKISCKASGYAFNYWLGWVKORPGHGLEW 300
 DB 241 GTTAVTSSGGGSDIKLQSGAEIVRPGTSVKISCKASGYAFNYWLGWVKORPGHGLEW 300
 QY 301 IGYINPSRGYNNYQKFDKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 360
 DB 301 IGYINPSRGYNNYQKFDKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 360
 QY 361 YWGQGTTLTVSS 372
 DB 361 YWGQGTTLTVSS 372

RESULT 8
 AD283629
 ID AD283629 standard; protein; 496 AA.

XX AC AD283629;
 XX DT 14-JUL-2005 (first entry)
 XX DE CD3 specific binding construct SEQ ID NO 251.

XX neoplasm; inflammation; immune disorder; infection; allergy;
 KM graft versus host disease; cytostatic; Antiinflammatory;
 KM Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
 XX Synthetic.
 OS
 XX WO2005040220-A1.
 PN
 XX 06-MAY-2005.
 PD
 XX 15-OCT-2004; 2004WO-EP011646.
 PF
 XX 16-OCT-2003; 2003EP-00023581.
 PR
 XX (MICR-) MICROMET AG.
 PA
 XX Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,
 PI Carr FU, Hamilton AA, Williams S;
 XX WPI; 2005-333494/34.
 DR N-PSDB; ADZ83628.
 XX
 PT New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT proliferative disease.
 PS Claim 20; SEQ ID NO 251; 639pp; English.
 XX
 XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a CD3 specific binding construct.
 XX
 SQ Sequence 496 AA;
 Query Match 92.5%; Score 1892; DB 9; Length 496;
 Best Local Similarity 93.5%; Pred. No. 5.6e-110;
 Matches 348; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
 QY 1 ELVMTGSSSLTVTAGEKVTMSCKSSQSLNSGNQKXLTWYQKPPQPKLLIYMASTR 60
 DB 1 ELVMTGSSSLTVTAGEKVTMSCKSSQSLNSGNQKXLTWYQKPPQPKLLIYMASTR 60
 QY 61 BSGVPDPTGSGSGDPTLTITSSVOABDLAVYVCONDYVPLTGAGTKLEIKGGGSGG 120
 DB 61 BSGVPDPTGSGSGDPTLTITSSVOABDLAVYVCONDYVPLTGAGTKLEIKGGGSGG 120
 QY 121 GSGSGGSEVOLLEBOSGAEIVRPGTSVXISCKASGYAFTNYMLGMVQKRPBGHEWIGDI 180
 DB 121 GSGSGGSEVOLLEBOSGAEIVRPGTSVXISCKASGYAFTNYMLGMVQKRPBGHEWIGDI 180
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMDWGQ 240
 DB 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMDWGQ 240
 QY 241 GTTWTVSAGGGGSGIYKLOOSGAELARPGASVMSCKTSYGFPTVTMVMVQKRGCGGLEW 300
 DB 241 GTTWTVSAGGGGSDVQLVQSGAEVAKKPGASVMSCKASGYFTFRTYTMHVMVQADPGGLEW 300

QY 301 IGYINPSRGYNTYNQFKOKATLTDDKSSSTAYWQLSLTFEDSAVYFCARRYDDHYCLD 360
 DB 301 IGYINPSRGYNTYNADSVKGRFTITDDKSSSTAYWQLSLTFEDSAVYFCARRYDDHYCLD 360
 QY 361 YMGQGTTLTVSS 372
 DB 361 YMGQGTTLTVSS 372
 RESULT 9
 ID ADZ83441
 ID ADZ83441 standard; protein; 515 AA.
 XX
 AC ADZ83441;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE Deimmunized construct 5-10xanti-CD3.
 XX
 KM neoplasm; inflammation; immune disorder; infection; allergy;
 KM graft versus host disease; cytostatic; Antiinflammatory;
 KM Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
 XX
 OS Synthetic.
 XX
 PN WO2005040220-A1.
 XX
 PD 06-MAY-2005.
 XX
 PF 15-OCT-2004; 2004WO-EP011646.
 PR
 XX 16-OCT-2003; 2003EP-00023581.
 PA (MICR-) MICROMET AG.
 PI Carr FU, Hamilton AA, Williams S;
 XX WPI; 2005-333494/34.
 DR N-PSDB; ADZ83440.
 XX
 PT New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT proliferative disease.
 PS Claim 20; SEQ ID NO 63; 639pp; English.
 XX
 XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of deimmunized construct 5-10xanti-CD3.
 XX
 SQ Sequence 515 AA;
 Query Match 92.5%; Score 1892; DB 9; Length 515;
 Best Local Similarity 93.5%; Pred. No. 5.8e-110;
 Matches 348; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
 QY 1 ELVMTGSSSLTVTAGEKVTMSCKSSQSLNSGNQKXLTWYQKPPQPKLLIYMASTR 60

Db 20 ELVWTPSSSLVTYAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 79
 Qy 61 ESGVPRFTSGSGCTDFTLTITSSVOAEDLAVYCCNDYSPPLTFGAGTKLEIKGGSGG 120
 Db 80 ESGVPRFTSGSGCTDFTLTITSSVOAEDLAVYCCNDYSPPLTFGAGTKLEIKGGSGG 139
 Qy 121 GSGGGGSEVQLLEQSGAELVRPCTSVKISCKASGAFYTWMLGMVQRPQHGLEMIGDI 180
 Db 140 GSGGGGSEVQLLEQSGAELVRPCTSVKISCKASGAFYTWMLGMVQRPQHGLEMIGDI 199
 Qy 181 FPGSGNIHNEKEFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMYWGQ 240
 Db 200 FPGSGNIHNEKEFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMYWGQ 259
 Qy 241 GTTVTVSSGGGSDIKLQSGAELARPASVYKMSCKTSGYTFTRYTMHWKORPGGLEW 300
 Db 260 GTTVTVSSGGGSDVQLVQSGAELKPKGASVYKMSCKASGYTFTRYTMHWKORPGGLEW 319
 Qy 301 IGYINPBRGYTNVYQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDHYCLD 360
 Db 320 IGYINPBRGYTNVADSVYKGRFTITTDKSTAYWQLSLTFEDSAVYFCARLYDDHYCLD 379
 Qy 361 YMGQGTTLTVSS 372
 Db 380 YMGQGTTLTVSS 391

RESULT 10
 AD283641
 ID AD283641 standard; protein, 496 AA.
 XX AC AD283641;
 DT 14-JUL-2005 (first entry)
 DE CD3 specific binding construct SEQ ID NO 263.
 XX neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW Immunosuppressive; Viroicide; Antibacterial; Antiallergic; Antiparasitic.
 XX Synthetic.
 OS WO2005040220-A1.
 PN 06-MAY-2005.
 PD 15-OCT-2004; 2004WO-EP011646.
 XX 16-OCT-2003; 2003EP-00023581.
 PR (MTCR-) MICROMET AG.
 PA Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,
 PI Carr FJ, Hamilton MA, Williams S;
 XX MPI, 2005-333494/34.
 DR N-PSDB; AD283640.
 XX New cytotoxicity active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.,
 PT proliferative disease.
 XX Claim 20; SEQ ID NO 263; 639pp; English.
 XX The invention relates to a cytotoxicity active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological

CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxicity active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a CD3 specific binding construct.

XX Sequence 496 AA;

Query Match 90.9%; Score 1859; DB 9; Length 496;

Best Local Similarity 71.6%; Pred. No. 6,4e-108; Matches 355; Conservative 11; Mismatches 6; Indels 124; Gaps 1;

Qy 1 ELVWTPSSSLVTYAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
 Db 1 ELVWTPSSSLVTYAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
 Qy 61 ESGVPRFTSGSGCTDFTLTITSSVOAEDLAVYCCNDYSPPLTFGAGTKLEIKGGSGG 120
 Db 61 ESGVPRFTSGSGCTDFTLTITSSVOAEDLAVYCCNDYSPPLTFGAGTKLEIKGGSGG 120
 Qy 61 IGYINPBRGYTNVYQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDHYCLD 180
 Db 61 IGYINPBRGYTNVADSVYKGRFTITTDKSTAYWQLSLTFEDSAVYFCARLYDDHYCLD 180
 Qy 121 GSGGGGSEVQLLEQSGAELVRPCTSVKISCKASGAFYTWMLGMVQRPQHGLEMIGDI 180
 Db 121 GSGGGGSEVQLLEQSGAELVRPCTSVKISCKASGAFYTWMLGMVQRPQHGLEMIGDI 180
 Qy 181 FPGSGNIHNEKEFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMYWGQ 240
 Db 181 FPGSGNIHNEKEFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMYWGQ 240
 Qy 241 GTTVTVSSGGGSDIKLQSGAELARPASVYKMSCKTSGYTFTRYTMHWKORPGGLEW 300
 Db 241 GTTVTVSSGGGSDIQTTPSSLSASVGRVITTCRASQSVSYMNYQKPKAPKWI 300
 Qy 241 GTTVTVSSGGGSDIQTTPSSLSASVGRVITTCRASQSVSYMNYQKPKAPKWI 300
 Db 241 GTTVTVSSGGGSDIQTTPSSLSASVGRVITTCRASQSVSYMNYQKPKAPKWI 300
 Qy 256
 Db 256
 Qy 301 YDTSKVASGVAPRFGSGSGCTDYSLTINSLEAEDLAAYYCCQMSNPPLTFGGTKVEIKG 360
 Db 301 YDTSKVASGVAPRFGSGSGCTDYSLTINSLEAEDLAAYYCCQMSNPPLTFGGTKVEIKG 360
 Qy 256
 Db 256
 Qy 361 EGTSTSGSGSGSGADVDVQLVQSGAELKPKGASVYKMSCKASGYTFTRYTMHWKORPGGLEW 420
 Db 361 EGTSTSGSGSGSGADVDVQLVQSGAELKPKGASVYKMSCKASGYTFTRYTMHWKORPGGLEW 420
 Qy 397 GLEWIGYINPBRGYTNVYQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDHYCLD 480
 Db 421 GLEWIGYINPBRGYTNVYQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDHYCLD 480
 Qy 357 YCLDYWGQGTTLTVSS 372
 Db 481 YCLDYWGQGTTLTVSS 496

RESULT 11
 AD283649
 ID AD283649 standard; protein, 496 AA.
 XX AC AD283649;
 DT 14-JUL-2005 (first entry)
 DE CD3 specific binding construct SEQ ID NO 271.
 XX neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW Immunosuppressive; Viroicide; Antibacterial; Antiallergic; Antiparasitic.
 XX Synthetic.
 OS WO2005040220-A1.
 PN 06-MAY-2005.
 PD 15-OCT-2004; 2004WO-EP011646.
 XX 16-OCT-2003; 2003EP-00023581.
 PR (MTCR-) MICROMET AG.
 PA Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,
 PI Carr FJ, Hamilton MA, Williams S;
 XX MPI, 2005-333494/34.
 DR N-PSDB; AD283640.
 XX New cytotoxicity active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.,
 PT proliferative disease.
 XX Claim 20; SEQ ID NO 263; 639pp; English.
 XX The invention relates to a cytotoxicity active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological

PF 15-OCT-2004; 2004WO-EP011646.
 XX
 PR 16-OCT-2003; 2003EP-00023581.
 XX
 PA (MICR-) MICROMET AG.
 XX
 PI Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baerle P,
 PI Carr FJ, Hamilton AA, Williams S;
 DR WPI; 2005-333494/34.
 DR N-PSDB; AD283648.
 XX
 PT New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an is-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.
 XX
 PS Claim 20; SEQ ID NO 271; 63pp; English.
 XX
 XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an is-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a CD3 specific binding construct.
 XX
 XX Sequence 496 AA;
 XQ

QY		357	YCLDPMGGGTTLVSS	372
			:	
Db		481	YCLDPMGGGTTLVSS	496
 RESULT 12				
ID	ADZ83657			
AC	ADZ83657			
DE	CD3 specific binding construct SEQ ID NO 279.			
XX	Synthetic.			
XX	WO2005040220-A1.			
XX	06-MAY-2005.			
XX	15-OCT-2004; 2004MO-EP011646.			
XX	16-OCT-2003; 2003EP-00023581.			
XX	(MIGR-) MICROMET AG.			
XX	Hofmeijer R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baerle P,			
XX	Carr FJ, Hamilton AA, Williams S;			
XX	WPI: 2005-333494/34.			
XX	N-PsDB; ADZ83656.			
XX	New cytotoxicity active CD3 specific binding construct comprises a first			
XX	domain specifically binding to human CD3 and an Ig-derived second binding			
XX	domain, useful for creating, preventing, or ameliorating, e.g.			
XX	proliferative disease.			
XX	Claim 20; SEQ ID NO 279; 639bp; English.			
XX	The invention relates to a cytotoxically active CD3 specific binding			
XX	construct comprising a first domain specifically binding to human CD3 and			
XX	an Ig-derived second binding domain. The CD3 specific binding construct			
XX	above or the construct produced by the process, nucleic acid molecule,			
XX	vector, or host is useful for the preparation of a pharmaceutical			
XX	composition for the prevention, treatment, or amelioration of a			
XX	proliferative disease, a tumor, an inflammatory disease, an immunological			
XX	disorder, an autoimmune disease, an infectious disease, viral disease,			
XX	allergic reactions, parasitic reactions, graft-versus-host diseases, or			
XX	host-versus-graft diseases. The cytotoxically active CD3 specific binding			
XX	construct is useful for treating, preventing, or ameliorating			
XX	proliferative disease, a tumor, an inflammatory disease, an immunological			
XX	disorder, an autoimmune disease, an infectious disease, viral disease,			
XX	allergic reactions, parasitic reactions, graft-versus-host diseases, or			
XX	host-versus-graft diseases. The present sequence represents the amino			
XX	acid sequence of a CD3 specific binding construct.			
XX	Sequence 496 AA:			
Query Match	90.9%	Score 1859;	DB 9;	Length 496;
Beef Local Similarity	71.6%	Pred. No. 6.4e-108;		
Matches 355;	Conservative 11;	Mismatches 6;	Indels 124;	Gaps 1
QY	1 ELVMTQSSTLTVTAGEKVTWSCSSOSGLNSGNOKNTLTYOQRGPCKLIIMASTR	60		
Db	1 ELVMTQSSTLTVTAGEKVTWSCSSOSGLNSGNOKNTLTYOQRGPCKLIIMASTR	60		
QY	61 ESGVDRTTGSQSGDTFTLTSSVOAEDLAIVYYCONDIYSPLTFAGTGLEIKGGGSGSG	120		

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Db      ||| 61 ESVGPRFTSGSGSDTLTITSSVOAEDLAVYCONDSYPLTGAAGTKLEIKGGGSGG 120
Qy      ||| 121 GSGSGGSEVOQLLEBOSGAELVRPGTSVKISCKASGYAFTNYMLGMVKORPGHGLEWIGDI 180
Db      ||| 121 GSGSGGSEVOQLLEBOSGAELVRPGTSVKISCKASGYAFTNYMLGMVKORPGHGLEWIGDI 180
Qy      ||| 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDDEPDYWGQ 240
Db      ||| 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDDEPDYWGQ 240
Qy      ||| 241 GTTYVSSGGGSGSI 255
Db      ||| 241 GTTYVSSGGGSGSDI VLTQSPATLSLSPGERATLTCRASSSVSYMMYQQKPKAPKMI 300
Qy      ||| 256 ----- 255
Db      ||| 301 YDTSKVASGVAPARRSGSGSDTDSITINSLEAEDAATYYCOQMSNPILTFGGGTKEIKG 360
Qy      ||| 256 -----KIQSGAELARPASVYMSCKTSGYTFRTYTMHMYKORPGQ 296
Db      ||| 361 EGTSTSGSGSGSGADVDVQLVQSGAEVKKPGASVKYSCKASGYFTFTYTMHMYRQAPGQ 420
Qy      ||| 297 GLEWIGYINPSRGYTNVYKFKDKATLTITDKSSSTAYWQLSLTFEDSAVYFCARLYDDH 356
Db      ||| 421 GLEWIGYINPSRGYTNVYKFKDKATLTITDKSSSTAYWQLSLTFEDSAVYFCARLYDDH 480
Qy      ||| 357 YCLDWYGGGTTLVSS 372
Db      ||| 481 YCLDWYGGGTTLVSS 496

RESULT 13
AD283436
ID AD283436 standard; protein; 515 AA.
XX
AC AD283436;
XX
DT 14-JUL-2005 (first entry)
XX
DE Deimmunized construct 4-1xanti-CD3.
XX
KW neoplasm; inflammation; immune disorder; infection; allergy;
KW graft versus host disease; Cytostatic; Antiinflammatory;
KW immunosuppressive; Virocide; Antibacterial; Antiallergic; Antiparasitic.
XX
OS Synthetic.
XX
PN WO2005040220-A1.
XX
PD 06-MAY-2005.
XX
PF 15-OCT-2004; 2004WO-EP011646.
XX
PR 16-OCT-2003; 2003EP-00023581.
XX
PA (MICR-) MICROMET AG.
XX
PI Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baerlele P;
PI Carr FU, Hamilton AA, Williams S;
XX
DR WPI; 2005-333494/34.
XX
DR N-PSDB; AD283435.
XX
PT New cytotoxicity active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
XX
PS Claim 20; SEQ ID NO 58; 639pp; English.
XX
CC The invention relates to a cytotoxicity active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and

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CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxicity active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of deimmunized construct 4-1xanti-CD3.
XX
SQ Sequence 515 AA;
XX
Query Match      89.4%; Score 1829; DB 9; Length 515;
Best Local Similarity 90.6%; Pred. No. 4.9e-106;
Matches 337; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Qy      1 ELVMTQSPSSSLTPTAGEKVTWISCKSSQSLNSGNQKNTLTYYQQKPGQPKLLIYMASTR 60
Db      20 ELVMTQSPSSSLTPTAGEKVTWISCKSSQSLNSGNQKNTLTYYQQKPGQPKLLIYMASTR 79
Qy      61 ESVGPRFTSGSGSDTDLTITSSVOAEDLAVYCONDSYPLTGAAGTKLEIKGGGSGG 120
Db      80 ESVGPRFTSGSGSDTDLTITSSVOAEDLAVYCONDSYPLTGAAGTKLEIKGGGSGG 139
Qy      121 GSGSGGSEVOQLLEBOSGAELVRPGTSVKISCKASGYAFTNYMLGMVKORPGHGLEWIGDI 180
Db      140 GSGSGGSEVOQLLEBOSGAELVRPGTSVKISCKASGYAFTNYMLGMVKORPGHGLEWIGDI 199
Qy      181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDDEPDYWGQ 240
Db      200 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDDEPDYWGQ 259
Qy      241 GTTYVSSGGGSDI KIQSGAELARPASVYMSCKTSGYTFRTYTMHMYKORPGHGLEW 300
Db      260 GTTYVSSGGGSDI KIQSGAELARPASVYMSCKTSGYTFRTYTMHMYKORPGHGLEW 319
Qy      301 IGYINPSRGYTNVYKFKDKATLTITDKSSSTAYWQLSLTFEDSAVYFCARLYDDH 360
Db      320 IGYINPSRGYTNVYKFKDKATLTITDKSSSTAYWQLSLTFEDSAVYFCARLYDDH 379
Qy      361 YWGGGTTLVSS 372
Db      380 YWGGGTTLVSS 391

RESULT 14
AD283619
ID AD283619 standard; protein; 496 AA.
XX
AC AD283619;
XX
DT 14-JUL-2005 (first entry)
XX
DE CD3 specific binding construct SEQ ID NO 241.
XX
KW neoplasm; inflammation; immune disorder; infection; allergy;
KW graft versus host disease; Cytostatic; Antiinflammatory;
KW immunosuppressive; Virocide; Antibacterial; Antiallergic; Antiparasitic.
XX
OS Synthetic.
XX
PN WO2005040220-A1.
XX
PD 06-MAY-2005.
XX
PF 15-OCT-2004; 2004WO-EP011646.
XX
PR 16-OCT-2003; 2003EP-00023581.

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XX (M1CR-) MICROMET AG.
XX
XX Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;
PI Carr FJ, Hamilton AA, Williams S;
XX
XX WPI; 2005-333494/34.
DR N-PSDB; ADZ83618.
XX
XX New cytotoxically active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
XX
XX Claim 20; SEQ ID NO 241; 639pp; English.
XX
XX The invention relates to a cytotoxically active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of a CD3 specific binding construct.
XX
SQ Sequence 496 AA;

Query Match 89.0%; Score 1821; DB 9; Length 496;
Best Local Similarity 70.4%; Pred. No. 1.5e-105;
Matches 349; Conservative 11; Mismatches 12; Indels 124; Gaps 1;
QY 1 ELVWTPSSSLTVTAGKRYMCKSSQSLNSGNQXNYLTWYQKPPKLLIYMASTR 60
DB 1 ELVWTPSSSLTVTAGKRYMCKSSQSLNSGNQXNYLTWYQKPPKLLIYMASTR 60
QY 61 ESVGPRFTSGSGGTDTLTITSSVOAEDLAVYYCONDYSPPLTFGAGTKLEIKGGGSGG 120
DB 61 ESVGPRFTSGSGGTDTLTITSSVOAEDLAVYYCONDYSPPLTFGAGTKLEIKGGGSGG 120
QY 121 GSGSGGSGSEVOLLEQSGAEIVRPQTSYKISCKASGYAFNTYWLGMVYKORPGHGLEWIGDI 180
DB 121 GSGSGGSGSEVOLLEQSGAEIVRPQTSYKISCKASGYAFNTYWLGMVYKORPGHGLEWIGDI 180
QY 181 PRSGNHYNKEFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMWQ 240
DB 181 PRSGNHYNKEFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMWQ 240
QY 241 GTTYSVSSGGGSDIQTWQSPSSLSASGVDRVITTCRASGSVSVMYQKPKAPKMI 300
DB 241 GTTYSVSSGGGSDIQTWQSPSSLSASGVDRVITTCRASGSVSVMYQKPKAPKMI 300
QY 256 ----- 255
DB 301 YDTSKVASGVPARFSGSGGTDTSLTINLEAEDAATYYCOQMSNPITFGGKTKEIKG 360
QY 256 -----KIQSGAEIARPGASVYKSCSTGTTFRYTHMYKORPGQ 296
DB 361 EGTSTGSGSGSGGADVDVLVOGSAEVKKEGASVYKSCASGYTFKRYTHMYKORPGQ 420
QY 297 GLEWIGYINPGRGYTNVQKFKDKATLTDDSSSTAYWQLSLTFSEDAVYFCARYYDDH 356
DB 421 GLEWIGYINPGRGYTNVQKFKDKATLTDDSSSTAYWQLSLTFSEDAVYFCARYYDDH 480
QY 357 YCLDYWGQGTTLTVSS 372
DB 357 YCLDYWGQGTTLTVSS 372

DB 481 YCLDYWGQGTTLTVSS 496
RESULT 15
ADZ83625 standard; protein; 496 AA.
XX
XX ADZ83625;
XX
XX 14-JUL-2005 (first entry)
DE CD3 specific binding construct SEQ ID NO 247.
XX
XX neoplasm; inflammation; immune disorder; infection; allergy;
KM graft versus host disease; cytostatic; Antiinflammatory;
KM immunosuppressive; Vitruicide; Antibacterial; Antiallergic; Antiparasitic.
XX
XX Synthetic.
OS
XX WO2005040220-A1.
XX
XX 06-MAY-2005.
XX
XX 15-OCT-2004; 2004MO-EP011646.
XX
XX 16-OCT-2003; 2003BP-00023581.
XX
XX (M1CR-) MICROMET AG.
XX
XX Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;
PI Carr FJ, Hamilton AA, Williams S;
XX
XX WPI; 2005-333494/34.
DR N-PSDB; ADZ83624.
XX
XX New cytotoxically active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
XX
XX Claim 20; SEQ ID NO 247; 639pp; English.
XX
XX The invention relates to a cytotoxically active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of a CD3 specific binding construct.
XX
SQ Sequence 496 AA;

Query Match 89.0%; Score 1821; DB 9; Length 496;
Best Local Similarity 70.4%; Pred. No. 1.5e-105;
Matches 349; Conservative 11; Mismatches 12; Indels 124; Gaps 1;
QY 1 ELVWTPSSSLTVTAGKRYMCKSSQSLNSGNQXNYLTWYQKPPKLLIYMASTR 60
DB 1 ELVWTPSSSLTVTAGKRYMCKSSQSLNSGNQXNYLTWYQKPPKLLIYMASTR 60
QY 61 ESVGPRFTSGSGGTDTLTITSSVOAEDLAVYYCONDYSPPLTFGAGTKLEIKGGGSGG 120
DB 61 ESVGPRFTSGSGGTDTLTITSSVOAEDLAVYYCONDYSPPLTFGAGTKLEIKGGGSGG 120

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QY 121 GCGGGGSEVOLLKSGAELVRFPGTSVKISCKASGYAFTNYWLGWVKORPGHGLEWIGDI 180
    |||||
Db 121 GCGGGGSEVOLLKSGAELVRFPGTSVKISCKASGYAFTNYWLGWVKORPGHGLEWIGDI 180
    |||||
QY 181 PFGSGNIHYNKEFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPEMDYWGQ 240
    |||||
Db 181 PFGSGNIHYNKEFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPEMDYWGQ 240
    |||||
QY 241 GTTVTVSSGGGSDI----- 255
    |||||
Db 241 GTTVTVSSGGGSDI VLTQSPATLSLSPERATLSCRASQSVSYVMNWYQOKPKAKPKMI 300
    |||||
QY 256 ----- 255
    |||||
Db 301 YDTSKVASGVPARFSGSGGTIDYSLTINSLEAEDATYYCOQWSNPPLTFGGGTVEIKG 360
    |||||
QY 256 -----KLOQSGAELARPQASYKMSCKTSGYTFETRYTMHWKORPGQ 296
    |||||
Db 361 EGTSTGSGSGSGGADVDVQLVQSGAEVKKPGASVKVSCKASGYTFTRITMHWKQAFGQ 420
    |||||
QY 297 GLEWIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYYCARYYDDH 356
    |||||
Db 421 GLEWIGYINPSRGYTNVADSVKGRFTITDDKSTSTAYMELSLRSEDTATYYCARYYDDH 480
    |||||
QY 357 YCLDYWGQGTITVSS 372
    |||||
Db 481 YCLDYWGQGTITVSS 496
    |||||

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 Job time : 91 secs

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